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(54) Title: HUMAN COLON CANCER ASSOCIATED GENE SEQUENCES AND POLYPEPTIDES

(57) Abstract

This invention relates to newly identified colon or colon cancer related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "colon cancer antigens", and to the complete gene sequences associated therewith and to the expression products thereof, as well as the use of such colon cancer antigens for detection, prevention and treatment of disorders of the colon, particularly the presence of colon cancer. This invention relates to the colon cancer antigens as well as vectors, host cells, antibodies directed to colon cancer antigens and recombinant and synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing disorders related to the colon, including colon cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of colon cancer antigens of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and/or function of the polypeptides of the present invention.

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Human Colon Cancer Associated Gene Sequences and Polypeptides

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Field of the Invention

This invention relates to newly identified colon or colon cancer related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "colon cancer antigens," and to the complete gene sequences 10 associated therewith and to the expression products thereof, as well as the use of such colon cancer antigens for detection, prevention and treatment of disorders of the colon, particularly the presence of colon cancer. This invention relates to the colon cancer antigens as well as vectors, host cells, antibodies directed to colon cancer antigens and recombinant and synthetic methods for producing the same. Also 15 provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing disorders related to the colon, including colon cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of colon cancer antigens of the invention. The present invention further relates to methods and/or compositions for 20 inhibiting the production and/or function of the polypeptides of the present invention.

Background of the Invention

Colorectal cancers are among the most common cancers in men and women in the U.S. and are one of the leading causes of death. Other than surgical resection no 25 other systemic or adjuvant therapy is available. Vogelstein and colleagues have described the sequence of genetic events that appear to be associated with the multistep process of colon cancer development in humans (Trends Genet 9(4):138-41 (1993)). An understanding of the molecular genetics of carcinogenesis, however, has not led to preventative or therapeutic measures. It can be expected that advances in 30 molecular genetics will lead to better risk assessment and early diagnosis but colorectal cancers will remain a deadly disease for a majority of patients due to the

lack of an adjuvant therapy. Adjuvant or systemic treatments are likely to arise from a better understanding of the autocrine factors responsible for the continued proliferation of cancer cells.

Colorectal carcinoma is a malignant neoplastic disease. There is a high 5 incidence of colorectal carcinoma in the Western world, particularly in the United States. Tumors of this type often metastasize through lymphatic and vascular channels.~~-Many patients with colorectal carcinoma eventually die from this disease. In fact, it is estimated that 62,000 persons in the United States alone die of colorectal carcinoma annually.~~

10 At the present time the only systemic treatment available for colon cancer is chemotherapy. However, chemotherapy has not proven to be very effective for the treatment of colon cancers for several reasons, the most important of which is the fact that colon cancers express high levels of the MDR gene (that codes for multi-drug resistance gene products). The MDR gene products actively transport the toxic 15 substances out of the cell before the chemotherapeutic agents can damage the DNA machinery of the cell. These toxic substances harm the normal cell populations more than they harm the colon cancer cells for the above reasons.

There is no effective systemic treatment for treating colon cancers other than 20 surgically removing the cancers. In the case of several other cancers, including breast cancers, the knowledge of growth promoting factors (such as EGF, estradiol, IGF-11) that appear to be expressed or effect the growth of the cancer cells, has been translated for treatment purposes. But in the case of colon cancers this knowledge has not been applied and therefore the treatment outcome for colon cancers remains bleak.

There is a need, therefore, for identification and characterization of such 25 factors that modulate activation and differentiation of colon cells, both normally and in disease states. In particular, there is a need to isolate and characterize additional molecules that mediate apoptosis, DNA repair, tumor-mediated angiogenesis, genetic imprinting, immune responses to tumors and tumor antigens and, among other things, that can play a role in detecting, preventing, ameliorating or correcting dysfunctions 30 or diseases of the colon.

Summary of the Invention

The present invention includes isolated nucleic acid molecules comprising, or alternatively, consisting of, a colon and/or colon cancer associated polynucleotide sequence disclosed in the sequence listing (as SEQ ID Nos:1 to 773) and/or contained 5 in a human cDNA clone described in Tables 1, 2 and 5 and deposited with the American Type Culture Collection ("ATCC"). Fragments, variant, and derivatives of these nucleic acid molecules are also encompassed by the invention. The present invention also includes isolated nucleic acid molecules comprising, or alternatively consisting of, a polynucleotide encoding a colon or colon cancer polypeptide. The 10 present invention further includes colon and/or colon cancer polypeptides encoded by these polynucleotides. Further provided for are amino acid sequences comprising, or alternatively consisting of, colon and/or colon cancer polypeptides as disclosed in the sequence listing (as SEQ ID Nos: 774 to 1546) and/or encoded by a human cDNA clone described in Tables 1, 2 and 5 and deposited with the ATCC. Antibodies that 15 bind these polypeptides are also encompassed by the invention. Polypeptide fragments, variants, and derivatives of these amino acid sequences are also encompassed by the invention, as are polynucleotides encoding these polypeptides and antibodies that bind these polypeptides. Also provided are diagnostic methods for diagnosing and treating, preventing, and/or prognosing disorders related to the colon, 20 including colon cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of colon cancer antigens of the invention.

Detailed Description

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Tables

Table 1 summarizes some of the colon cancer antigens encompassed by the invention (including contig sequences (SEQ ID NO:X) and the cDNA clone related to the contig sequence) and further summarizes certain characteristics of the colon 30 cancer polynucleotides and the polypeptides encoded thereby. The first column shows the "SEQ ID NO:" for each of the 773 colon cancer antigen polynucleotide sequences of the invention. The second column provides a unique "Sequence/Contig ID"

identification for each colon and/or colon cancer associated sequence. The third column, "Gene Name," and the fourth column, "Overlap," provide a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database and the database accession no. for the database sequence having similarity, respectively. The fifth and sixth columns provide the location (nucleotide position nos. within the contig), "Start" and "End", in the polynucleotide sequence "SEQ-ID-NO:X" that delineate the preferred ORF shown in the sequence listing as SEQ ID NO:Y. The seventh and eighth columns provide the "% Identity" (percent identity) and "% Similarity" (percent similarity), respectively, observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence. The ninth column provides a unique "Clone ID" for a cDNA clone related to each contig sequence.

Table 2 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

Table 3 indicates public ESTs, of which at least one, two, three, four, five, ten, fifteen or more of any one or more of these public EST sequences are optionally excluded from certain embodiments of the invention.

Table 4 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in most of the colon or colon cancer associated polynucleotides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power Macintosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). Colon and colon cancer associated polypeptides shown in Table 1 may possess one or more antigenic epitopes comprising residues described in Table 4. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown in Table 4 correspond to the amino acid sequences for most colon and colon cancer associated polypeptide sequence shown in the Sequence Listing.

Table 5 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

- 5 In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.
- 10
- 15

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X (as described in column 1 of Table 1) or the related cDNA clone (as described in column 9 of Table 1 and contained within a library deposited with the ATCC). For example, the polynucleotide can contain the 20 nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

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In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human 30 Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown in column 9 of Table 1, each clone is identified by a cDNA Clone ID. Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to

retrieve a given clone from the HGS library. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 5 provides a list of the deposited cDNA libraries. One can use the Clone ID to 5 determine the library source by reference to Tables 2 and 5. Table 5 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA 10 clone ("Clone ID") isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1 correlates the Clone ID names with SEQ ID NOs. Thus, starting with a SEQ ID NO, one can use Tables 1, 2 and 5 to 15 determine the corresponding Clone ID, from which library it came and in which ATCC deposit the library is contained. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms 20 for the purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to 25 sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), and/or sequences contained in the related cDNA clone within a library deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

Also included within "polynucleotides" of the present invention are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower 30 stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt

conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 5 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

- Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress 10 background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.
- 15 Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically 20 any double-stranded cDNA clone generated using oligo dT as a primer).

The polynucleotides of the present invention can be composed of any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double- 25 stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A 30 polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of

modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

"SEQ ID NO:X" refers to a colon cancer antigen polynucleotide sequence described in Table 1. SEQ ID NO:X is identified by an integer specified in column 1 of Table 1. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. There are 773 colon cancer antigen polynucleotide sequences described in Table 1 and shown in the sequence listing (SEQ ID NO:1 through SEQ ID NO:773). Likewise there are 773 polypeptide sequences shown in the sequence listing, one polypeptide sequence for each of the polynucleotide sequences (SEQ ID NO:774 through SEQ ID NO:1546). The polynucleotide sequences are shown in the sequence listing immediately followed by all of the polypeptide sequences. Thus, a polypeptide sequence corresponding to polynucleotide sequence SEQ ID NO:1 is the first polypeptide sequence shown in the sequence listing. The second polypeptide sequence corresponds to the polynucleotide sequence shown as SEQ ID NO:2, and so on. In otherwords, since there are 773 polynucleotide sequences, for any polynucleotide sequence SEQ ID NO:X, a corresponding polypeptide SEQ ID NO:Y can be determined by the formula X + 773 = Y. In addition, any of the unique "Sequence/Contig ID" defined in column two of Table 1, can be linked to the corresponding polypeptide SEQ ID NO:Y by reference to Table 4.

The polypeptides of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids.

5 The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same

10 type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or

15 15 may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination.

20 20 (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

25 30 The colon and colon cancer polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced

polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

- 5 It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.
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- The colon and colon cancer polypeptides of the present invention are
10 preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from
15 natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the polypeptides of the present invention in methods which are well known in the art.

- By a polypeptide demonstrating a "functional activity" is meant, a polypeptide
20 capable of displaying one or more known functional activities associated with a full-length (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to
25 form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

- "A polypeptide having functional activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular assay, such as,
30 for example, a biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to

the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

- 5 The functional activity of the colon cancer antigen polypeptides, and fragments, variants derivatives, and analogs thereof, can be assayed by various methods.
-

For example, in one embodiment where one is assaying for the ability to bind or compete with full-length polypeptide of the present invention for binding to an antibody to the full length polypeptide antibody, various immunoassays known in the art can be used, including but not limited to, competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

In another embodiment, where a ligand is identified, or the ability of a polypeptide fragment, variant or derivative of the invention to multimerize is being evaluated, binding can be assayed, e.g., by means well-known in the art, such as, for example, reducing and non-reducing gel chromatography, protein affinity chromatography, and affinity blotting. See generally, Phizicky, E., et al., Microbiol. Rev. 59:94-123 (1995). In another embodiment, physiological correlates polypeptide of the present invention binding to its substrates (signal transduction) can be assayed.

In addition, assays described herein (see Examples) and otherwise known in the art may routinely be applied to measure the ability of polypeptides of the present

invention and fragments, variants derivatives and analogs thereof to elicit polypeptide related biological activity (either in vitro or in vivo). Other methods will be known to the skilled artisan and are within the scope of the invention.

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Colon and Colon Cancer Associated Polynucleotides and Polypeptides of the Invention

It has been discovered herein that the polynucleotides described in Table 1 are expressed at significantly enhanced levels in human colon and/or colon cancer tissues.

- 10 Accordingly, such polynucleotides, polypeptides encoded by such polynucleotides, and antibodies specific for such polypeptides find use in the prediction, diagnosis, prevention and treatment of colon related disorders, including colon cancer as more fully described below.

- 15 Table 1 summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and the related cDNA clones) and further summarizes certain characteristics of these colon and/or colon cancer associated polynucleotides and the polypeptides encoded thereby.

Table 1

Seq ID No.	Sequence/ Contig ID	Gene Name	Overlap	HGS Nucleotide Start	HGS Nucleotide End	% Identity	% Similarity	Clone ID
1	500802			2	304			HGBA183
2	531091			2	292			HUKDY21
3	553147	immunoglobulin kappa light chain variable region L25 [Homo sapiens] >pir S41816 S41816 Ig kappa chain V region L25 - human Length = 119	g 415381	3	440	73	86	HCASG85
4	558860	(AB008790) Grb7V protein [Homo sapiens] >sp D1030000 D1030000 GRB7V PROTEIN. >g 1526535 Grb7 protein [Homo sapiens] {SUB 130-343}; Length = 447	gnl PID d1030000	33	635	97	98	HCEGY28
5	561730	(AF039700) antigen NY-CO-38 [Homo sapiens] >sp G3170200 G3170200 ANTIGEN NY-CO-38. >g 3170198 (AF039699) antigen NY-CO-37 [Homo sapiens] {SUB 1-403} Length = 652 MDA-7 [Homo sapiens] >sp Q13007 MDA7_HUMAN MDA-7 PROTEIN PRECURSOR (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 7). Length = 206	g 3170200	34	393	98	98	HSDF4A48
6	585938	MDA-7 [Homo sapiens] >sp Q13007 MDA7_HUMAN MDA-7 PROTEIN PRECURSOR (MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN 7). Length = 206 disintegrin-protease [Homo sapiens]	g 1141751	206	538	81	81	HMQBR31
7	587785	>sp O15204 O15204 DISINTEGRIN- PROTEASE. Length = 470	gnl PID e332729	2	331	100	100	IIOSB086

8	588916	Human apoC-II gene for preproapolipoprotein C-II [Homo sapiens] >gi 757915 apocII protein [Homo sapiens] >gi 178836 apolipoprotein C-II [Homo sapiens] >pir A24238 LP-IUC2 apolipoprotein C-II precursor - human	gi 296636	5	376	100	100	HLDQUS6
9	613825			3	260			HMSHIB03
10	639090			254	559			HCRME22
11	651644			63	194			HCFB073
12	659544			109	249			HJMBUIS
13	659739	KHS1 [Homo sapiens] >sp G185733 G1857331 KHS1. Length = 846	gi 1857331	238	1140	94	94	HSYAM68
14	661057	protein kinase Dyrk2 [Homo sapiens] >sp Q92630 Q92630 PROTEIN KINASE DYRK2 (PROTEIN KINASE, DYRK2). >gnl PID e280618 Dyrk2 [Homo sapiens] {SUB 320-528} Length = 528	gnl PID e321513	3	425	100	100	HCDBBX83
15	661313			894	1118			HHEMN11
16	666316			193	369			HCDCH84
17	669229			430	762			HOHDD51
18	670471	(AJ003061) most expressed alternative spliced form [Homo sapiens] >sp Q60832 Q60832 PROTEIN ENCODED BY SACCHAROMYCES CEREVISIAE SPC98 HOMOLOGUE. Length = 907	gnl PID e1293754	203	937	92	93	HAGGX21
19	676611							HCE5C73
	691240							HIISAN54
						207	530	
						2	385	

21	702977	26-kDa cell surface protein TAPA-1 [Homo sapiens] >pir A35649 A35649 cell surface protein TAPA-1 - human >sp P18582 CD81_HUMAN CD81 ANTIGEN (26 KD CELL SURFACE PROTEIN TAPA-1). Length = 236	gi 338678	34	819	80	80	HGCMV09
22	709517	(AF062476) retinoic acid-responsive protein; STRA6 [Mus musculus] >sp O70491 O70491 RETINOIC ACID- RESPONSIVE PROTEIN. Length = 670	gi 3126975	344	478	75	88	HWLJX38 HCRND05
23	714730	(AF076856) small espin [Rattus norvegicus] >sp G3818569 G3818569 SMALL ESPIN. Length = 253	gi 3818569	530	886	62	64	HAPIL75 HCEOQ15 HWLFA47
24	714834	(AF076856) small espin [Rattus norvegicus] >sp G3818569 G3818569 SMALL ESPIN. Length = 253	gi 3818569	530	886	62	64	HAPIL75 HCEOQ15 HWLFA47
25	715016	muskelin [Mus musculus] >sp O89050 O89050 MUSKELIN.	gi 3493462	1	444	92	95	HUSXP30
26	719584	Length = 735 (AB015318) gamma2-adaptin [Homo sapiens] >sp C75843 O75843 GAMMA2-ADAPTIN. Length = 785	gn PID d1034356	160	801	100	100	HBIG25
27	724637	similar to ADP-ribosylation factor; (AF054179) II beta 58 homolog [Homo sapiens] >sp O75436 O75436_II BEta 58 HOMOLOG. Length = 327	gn PID e1350748	137	289	87	97	HCRMQ71 HSDZB27
28	728392	similar to ADP-ribosylation factor; (AF054179) II beta 58 homolog [Homo sapiens] >sp O75436 O75436_II BEta 58 HOMOLOG. Length = 327	gi 3342000	2	502	87	97	HKABV36
29	738716							
30	739056							
31	739143							
32	742329							
33	742557							
34	745481							
35	746035							
36	7533731							

37	754383	3	434	HBGMG69
38	756749	3	464	HMEIZ19
39	757980	365	622	HETIS94
40	764818	3	1700	HCE4A59
41	765140	3	200	HRODG74
42	766893	178	414	HCEOS64
43	771338	(AF034745) LNXP80 [Mus musculus] >sp O70263 O70263 LIGAND OF NUMB-PROTEIN X (LNXP80). Length = 728	1	96
44	771412	g 2352906	2	HCHAG61
45	772226	(AF011794) cell cycle progression restoration 8 protein [Homo sapiens] >sp Q14712 Q14712 CELL CYCLE PROGRESSION RESTORATION 8 PROTEIN. Length = 375	3	HMVCR68
46	773057		36	HE2BE05
47	773173		514	HTEPE82
48	780154		44	HCEZW82
49	780768		820	HPLBS64
50	780779	similar to G9a gene. [Homo sapiens] >sp Q15047 Q15047 mRNA (KIAA0067) FOR ORF (RELATED TO G9A GENE), COMPLETE CDS (KIAA0067). Length = 1291	1176	HAMFL51
51	782394	g 1007261	134	86
52	783160	(AF026977) microsomal glutathione S- transferase 3 [Homo sapiens] >sp O14880 O14880 MICROSOMAL GLUTATHIONE S-TRANSFERASE 3. Length = 152	658	86
53	783506		1068	1337
		g 23583081	25	100
			492	100
			49	825
				HODCW56

54	784446		19	282	H3HCL85
55	784832		134	751	HCGM184
56	786813		114	347	HE2O155
57	792139	(AB002086) p47 [Rattus norvegicus] >gnl PID e294068 XY40 protein [Rattus norvegicus] >sp Q35987 Q35987 P47, COMPLETE CDS. Length = 370	32	334	H6EEC65
58	793987		100	564	HCIAE18
59	805715		513	1226	HDPK164
60	811111		1	438	HCEDF72
61	811113	steroidogenic acute regulatory protein [Mus musculus] >pir A55455 A55455 steroidogenic acute regulatory protein precursor, mitochondrial - mouse Length = 284	2	718	HWBEX78
62	823902	(AF028722) fetal globin inducing factor [Mus musculus] >sp G4103857 G4103857 FETAL GLOBIN INDUCING FACTOR. Length = 238	36	497	HDTBD43
63	826518	RNase 4 [Homo sapiens] >pir S2489 S2489 ribonuclease 4 (EC 3.1.-.) precursor - human Length = 147	1	231	HLQCQ62
64	826704		475	726	HCQBI18
65	827720		789	1076	HFICY86
66	828102	(AB013456) aquaporin 8 [Homo sapiens] >gnl PID d1035202 (AB013456)	106	297	HSRFC02
67	828180	aquaporin 8 [Homo sapiens] >sp D1035202 D1035202 AQUAPORIN 8. Length = 261	20	883	IIWLFM26

68	828386	(AF093821) RRM RNA binding protein GRY-RBP [Mus musculus] >sp O88991 O88991 RRM RNA BINDING PROTEIN GRY-RBP. Length = 625	gi 3694986	3	650	100	100	HOHAD26
69	828658	protein-tyrosine-phosphatase [Homo sapiens] >gnl PID d1032930 (AB013601) DUSP6 [Homo sapiens] >gnl PID d1035350 (AB013382) DUSP6 [Homo sapiens] >gnl PID d1032930 (AB013601) DUSP6 [Homo sapiens] >sp Q16828 DUS6_HUMAN DUAL SPECIFICITY PROTEIN PHOSPHATASE 6	gnl PID e218263	2	568	100	100	HLHCO24
70	828919	RNA helicase [Homo sapiens] >pir S71758 S71758 DEAD box protein MrDb, Myc-regulated - human >sp Q92732 Q92732 RNA HELICASE. Length = 610	gnl PID e254454	2	661	99	100	HFOYL30
71	829572							
72	830138	similar to Glyoxalase [Caenorhabditis elegans] Length = 281	gnl PID e1344082	134	163	411	53	HSVAK51 HYAAH90
73	830208	UbCHSB [Homo sapiens] >gi 595668 ubiquitin conjugating enzyme [Rattus norvegicus] >gi 480742 ubiquitin conjugating enzyme [Mus musculus] >pir SS33359 SS3359 ubiquitin conjugating enzyme (E217kB) - rat Length = 147	gi 1145689	2	205	92	95	HBNCN46
74	830248	A33 antigen precursor [Homo sapiens] >sp Q99795 A33_HUMAN CELL SURFACE A33 ANTIGEN	gi 1814277	3	1097	30	39	HWLHJ3

PRECURSOR. Length = 319

75	830275	Similar to D.melanogaster parallel sister chromatids protein [Homo sapiens]>sp Q92549 Q92549 MYELOBLAST K1AA0261 (FRAGMENT). Length = 1287	gn PIDd1014081	3	647	100	100	HWLFO28
76	830286	interferon-related putative protein [Homo sapiens]>sp Q12894 Q12894 HYPOTHETICAL_48.0 KID PROTEIN.>gi 1209022 interiferon-related putative protein [Homo sapiens] {SUB 2-442} Length = 442	gi 2880033	385	1488	91	91	HWLFE46
77	830347	(AF039401) calcium-dependent chloride channel-1 [Homo sapiens]>sp G4009460 G4009460 CALCIUM-DEPENDENT CHLORIDE CHANNEL-1. Length = 914	gi 4009460	3	656	63	76	HWLEL81
78	830348	inorganic pyrophosphatase (EC 3.6.1.1) - pir A45153 A4515	3	911				HWHQR45
79	830364	bovine >sp P37980 IPYR_BOVIN INORGANIC PYROPHOSPHATASE (EC 3.6.1.1)(PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE). Length = 289	3	1022	67	85		HWLEI47
80	830394			1	951			HDPPVF62
81	830398			526	627			HWBCR84

82	830412	SDF2 [Homo sapiens] >pir C5106 JC5106 stratal cell-derived factor 2 - human >spi Q99470 Q99470 SDF2. Length = 211	gn PID d1009953	233	928	91	92	HWHHQ57
83	830436	(AJ005821) X-like 1 protein [Homo sapiens] >spi E1291794 E1291794 X- LIKE 1 PROTEIN. Length = 3027	gn PID e1291794	83	523	65	78	HWABR83
84	830464	CLP36 [Rattus norvegicus] >pir JC4385 JC4385 LIM protein - rat >spi P52944 CL36_RAT LIM PROTEIN CLP36. Length = 327	gi 020151	2	289	72	81	HUSGB72
85	830471	(AF011794) cell cycle progression restoration 8 protein [Homo sapiens] >spi O14712 O14712 CELL CYCLE PROGRESSION RESTORATION 8 PROTEIN. Length = 375	gi 2352906	95	229	95	96	HUSIK51
86	830477	ORF YGR036c [Saccharomyces cerevisiae] >pir S64327 S64327 probable membrane protein YGR036c - yeast (Saccharomyces cerevisiae) Length = 239	gn PID e243385	185	736	38	54	HJPCP29
87	830500	(AL021813) phenylalanyl-tRNA synthetase alpha chain [Schizosaccharomyces pombe] >spi O42849 O42849 PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN. Length = 589	gn PID e1250585	2	1081	40	63	HUFAU68
88	830509	(AL021813) phenylalanyl-tRNA synthetase alpha chain [Schizosaccharomyces pombe] >spi O42849 O42849 PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN. Length = 589						

101	830778	methionine aminopeptidase [Homo sapiens] >gi 687243 eIF-2-associated p67 homolog [Homo sapiens] >pir S52112 DPHUM2 methionyl aminopeptidase (EC 3.4.11.18) 2 - human >sp P50579 AMP2_HUMAN METHIONINE AMINOPEPTIDASE 2 (EC 3.4.11.18) (METAP 2) (PEPTIDASE M 2)	gi 903982	26	718	99	100	HSPAX18
102	830784	(AF039918) CD39L4 [Homo sapiens]	gi 3335102	595	858	94	94	HSIFY77 HHPDD94
103	830800	>sp O75356 O75356 CD39L4. Length = 428		1	990			HAQND53 HHEAA48 HPJCT75 HPIBH48
104	830821			449	754			
105	830849			464	868			
106	830903	tumor necrosis factor type I receptor associated protein [Homo sapiens] >pir A55877 A55877 tumor necrosis factor type I receptor associated protein	gi 687237	1	525			
107	830913	TRAP-I - human microsomal glutathione S-transferase 2 [Homo sapiens] >sp Q99735 GST2_HUMAN		3	1193	99	99	
108	830920	MICROSOMAL GLUTATHIONE S-TRANSFERASE II (EC 2.5.1.18) (MICROSOMAL GST-II). Length = 147 peroxisome proliferator activated receptor gamma 2 [Homo sapiens] >gi 1711117 ligand activated transcription factor PPARgamma2 [Homo sapiens]	gi 1747521	90	650	87	87	HIPHA84
109	830938		gi 1432177	227	610	98	98	HONAE45

110	830980	beta COP [Rattus norvegicus] >pir S13520 S13520 beta-COP protein - rat >sp P23514 [COPB_RAT] COATOMER BETA SUBUNIT (BETA- COAT PROTEIN)(BETA-COP).	gi 55819	47	289	95	98	HCESG53
111	831014	>pir S13636 S13636 110K protein - rabbit {SUB 451-500} Length = 953 >pir S13636 S13636 110K protein - rabbit {SUB 451-500} Length = 953 (AF016687) similar to alpha-actinin [Caenorhabditis elegans] >sp O16785 O16785 T21D12.4 PROTEIN. Length = 375	gi 2315828	310	1188	53	73	HOEBV08
112	831026			340	687			HOBAAE30
113	831031			526	765			HTXOK56
114	831055	(AF091395) Trio isoform [Homo sapiens]>sp O75962 O75962 TRIO ISOFORM. Length = 3038	gi 3644048	674	1921	93	94	HNTAT24
115	831057			3	1106			HNTCW73
116	831062			3	821			HNTBD04
117	831117			400	579			HMWBR70
118	831122	cell surface glycoprotein [Homo sapiens] >gi 567110 Human CD79b/Ig beta/B29 gene, complete coding sequence.], gene product [Homo sapiens]>bbs I22035 membrane immunoglobulin beta chain, Ig-beta=Ag receptor complex [human, B cells. Peptide, 229 aal [Homo	gi 179312	2	772	91	92	HMWCV70
119	831125					868	1023	HMWFH12
120	831132					36	185	HMUAR55

121	831152	(AC004668) similar to murine cell cycle regulator MID1; similar to A57591 (PID:g2137417) [Homo sapiens]>sp O60414 O60414	gi 3115346	111	875	90	91	HMVA157
122	831157	WUGSC:H_RG276C03_1A PROTEIN (FRAGMENT) Length = 635 (AF030109) regulator of G protein signaling 12 [Homo sapiens]>gi 2766633 (AF030152) regulator of G protein signaling 12 [Homo sapiens] Length = 799	gi 2605780	664	1110	100	100	HMVAA24
123	831160	ezrin (AA 1-586) [Homo sapiens]>pir A34400 A34400 ezrin - human>sp P15311 EZRI_HUMAN EZRIN (P81) (CYTOVILLIN) (VILLIN-2).{SUB 2-586}>gi 340217 cytovillin 2 [Homo sapiens] {SUB 12-586} Length = 586	gi 31283	3	1907	100	100	HCRPE60
124	831193				256	378		IMIAG77
125	831197				884	1267		HMELOQ02
126	831217				152	427		HTAAN07
127	831239				420	638		HAKBB67
128	831248				84	443		HCFLL08
129	831313	c-fos protein [Homo sapiens]>gi 29904 c-fos gene product [Homo sapiens]>gi 4063509 (AF111167) cfos [Homo sapiens]>pir A01342 TVHUF1 transforming protein fos - human>sp P01100 FOS_HUMAN P55-C-FOS PROTO-ONCOGENE PROTEIN (G0S7 PROTEIN).>sp G4063509 G406	gi 182735	1182	1670	83	88	HAGDZ30
130	831369				31	1464		HDQFB94

131	831371	cytochrome P450j [Homo sapiens] >gi 181356 cytochrome P450jE1 [Homo sapiens] >pir A31949 A31949					
132	831373	cytochrome P450 21,1 - human >sp P0518 CPE1_HUMAN CYTOCHROME P450 21E1 (EC 1.14.14.1) (CYP11E1) (P450-1). P4501E1 [Homo sapiens]	g 181360	81	344	94	HLADA ²⁸ HWADP ⁴⁷
				221	1744	94	
133	831387	hydroxymethylglutaryl-CoA synthase [Homo sapiens] >gi 2463646 3-hydroxy- 3-methylglutaryl CoA synthase [Homo sapiens] >pir S7 623 S7 623 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) precursor, mitochondrial - human >sp P54868 IMCM_HUMAN HYDROXYMETHYLGLU	g 619877	717	1586	100	HWLLY ⁴⁵
134	831410	mucin_2 precursor, intestinal - human (fragments) >gi 186396 mucin [Homo sapiens] {SUB 626-1895} >gi 186398 MUC2 [Homo sapiens] {SUB 2037- 3020} >gi 188874 intestinal mucin [Homo sapiens] {SUB 1916-2193} >gi 188615 mucin-like protein [Homo sapiens] {SUB 23}	pir A49963 A4393	2	727	95	HCQDM ²³
				2			
135	831448	calcium-modulated protein S100-beta [artificial sequence] >pir A91254 BCBO1B S-100 protein beta chain - bovine {SUB 2-92} Length = 92	g 554574	126	482	32	HKACO ⁸¹
136	831450						IJKABKSS
						807	1319

145	831594	protein serine/threonine kinase [Homo sapiens]>gi 468789 CDK activating kinase [Homo sapiens]>gi 485909 MO15/CDK-activating kinase (CAK) [Homo sapiens]>gnl PID e257806 Cdk-activating kinase [Homo sapiens]>pir A54820 A54820 CDK-activating protein kinases	gi 348243	117 23	677 802	99 99	HHECU01 HHEDO14
146	831598	translational initiation factor beta subunit [Homo sapiens]>pir A31226 A31226 translation initiation factor eIF-2 beta chain - human >pir S13147 S13147 protein synthesis factor - rabbit >sp P20042 IF2B_HUMAN	gi 182067	120	1154	87	HI-IEFB46
147	831608	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BET	gi 854124	3	104	96	EISAU33
148	831613	Human giant larvae homologue [Homo sapiens]>pir S55474 S55474 Human giant larvae homology - human >sp Q14521 Q14521 GIANT LARVAE HOMOLOGUE. Length = 1015 alpha I-acid glycoprotein [Homo sapiens]>gi 340138 alpha I-acid glycoprotein [Homo sapiens] {SUB 39-86} Length = 201	gnl PID e222211	46	690	99	HGBBLZ56

156	831741	myelodysplasia/myeloid leukemia factor 2 [Homo sapiens]>gi 3381897 (AF070539) myelodysplasia/myeloid leukemia factor 2 [Homo sapiens]	gi 1399745	186	974	77	77	HFEBT03
157	831754	MYELODYSPLASIA/MYELOID LEUKEMIA FACTOR 2. Length = 248 multidrug resistance protein 3 [Homo sapiens] >gi PID e1288198 multidrug resistance protein 3 [Homo sapiens] >gi PID e1288198 multidrug resistance protein 3 [Homo sapiens] >sp O60922 O60922 MULTIDRUG RESISTANCE PROTEIN 3. Length = 1526	gn PID e1288198	1	924	92	92	HWMEZ67
158	831760			373	510			HETEH76
159	831780			2	1003			HELGH58
160	831796				1158			HE9RY54
161	831800	nuclear protein SA-2 [Homo sapiens]>sp O00540 O00540 NUCLEAR PROTEIN SA-2. Length = 1162	gn PID e250094	600	1541	93	93	HFIAU59
162	831807			1015	1341			HE9QD17
163	831812			520	765			HE9QY91
164	831813			83	793			HEAHA84
165	831830	isoleucyl-tRNA synthetase [Homo sapiens] >pir 59314 59314 isoleucine-tRNA ligase (EC 6.1.1.5) - human Length = 1266	gn PID d1006382	52	2307	98	99	HE8TV13
166	831860	Similarity to S. Pombe BEM1/BUDS suppressor;	gn PID e1347870	465	776	69	84	HE8OT93
167	831872			1	1671			HE8CL14
168	831896			1	2121			HDTDX05

169	831928	(AF061795) dynamin-like protein Dymple isoform [Homo sapiens] >sp O60709 O60709 DYNAMIN-LIKE PROTEIN DYMPL E ISOFORM. Length = 699	gi 3126874	2	778	77	77	HSYB086
170	831949			3	1109			HE8TX12
171	831950			48	521			HAPQSS1
172	831953	carbonic anhydrase II [Homo sapiens] >gi 179780 carbonic anhydrase II [Homo sapiens]>gi 179795 carbonic anhydrase II [Homo sapiens]>gi 29587 carbonic anhydrase II (AA 1-260) [Homo sapiens]	gi 179772	106	987	100	100	HWLHA60
173	831975			555	761			HDTB006
174	832036	human phosphotyrosine phosphatase kappa [Homo sapiens] Length = 1439	gn PID e234080	2	490	82	82	HCYAC13
175	832047			877	1137			HCWK885
176	832078			751	1014			HASABI4
177	832100			687	917			HCRNM09
178	832104			95	220			HCRMU71
179	832268			18	191			HTXOU56
180	832270	Ca2+ ATPase of fast-twitch skeletal muscle sarcoplasmic reticulum, adult isoform [Homo sapiens] >sp O14983 O14983 CA2+ ATPASE OF FAST-TWITCH SKELETAL MUSCLE SACROPLASMIC RETICULUM, ADULT ISOFORM. Length = 1001	gi 2052522	622	1290	90	91	HBKDW03

181	832279	acetyl-CoA synthetase [Drosophila melanogaster] >pir SS2154 S52154 acetyl-CoA synthetase - fruit fly (Drosophila melanogaster) >sp Q24226 Q24226 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE (ACYL-ACTIVATING ENZYME). Length = 381	gi 608694	2	1237	65	77	HIBKDN33
182	832317	11kD protein [Homo sapiens] Length = 111	gi 897917	270	719	100	100	HBIAX17
183	832354	sialidase [Homo sapiens] >gi 2773339 (AF040958) lysosomal neuraminidase precursor [Homo sapiens] >gi 4099141 lysosomal sialidase [Homo sapiens]	gn PID e303801	1	408	3	1385	HBBBE52
184	832364	>sp Q99511 Q99519 SIALIDASE PRECURSOR. >sp [G4099141 G4099141 LYSSOSOMAL SIALIDASE		3	746	96	96	HDPPQA93
185	832378	LYSSOSOMAL SIALIDASE PRECURSOR (EC 3.2.1.18). Length = 86						HATC072
186	832385	[Homo sapiens] >sp O60575 O60575 GASTROINTESTINAL PEPTIDE. Length = 335	gi 2935440	2	316	90	90	HARAG42
187	832428	APO-1 ANTIGEN, FAS ANTIGEN. Length = 335	sp G249613 G249613	136	846	97	97	HAMGD53
188	832485			202	597			HAGHC54

189	832494	Ku protein subunit [Homo sapiens] >gi 178650 p70 autoantigen [Homo sapiens]>gi 339667 thyroid autoantigen [Homo sapiens]>bbs J07206 Ku autoantigen p70 subunit [human, Peptide, 609 aa] [Homo sapiens] >pir A30299 A30894 70K thyroid autoantigen - human >sp	gi 307095 80 Similar to Human C219-reactive peptide (L34688) [Homo sapiens] >sp Q92580 Q92580 MYELOBLAST KIA0268 (FRAGMENT).>gi 511639 C219-reactive peptide [Homo sapiens] {SUB 592-727} Length = 1193	gn PID d1014138 3 Similar to Human C219-reactive peptide (L34688) [Homo sapiens] >sp Q92580 Q92580 MYELOBLAST KIA0268 (FRAGMENT).>gi 511639 C219-reactive peptide [Homo sapiens] {SUB 592-727} Length = 1193	1058 3 Length = 1067	87 87 Length = 1067	90 90 Length = 1067	90 90 Length = 1067	HAIBY70 HDPTT16 HCRPH70
190	832512	integrin alpha6 subunit [Homo sapiens] Length = 1067	gi 33942 2 Length = 1067	gi 33942 2 Length = 1067	1660	96	96	96	HADCX04
191	832515	nuclear factor RPI40 [Homo sapiens] >pir S57348 S57348 nuclear factor RPI40 - human Length = 1158	gi 940539 34 protein tyrosine kinase [Homo sapiens] >pir A55922 A55922 tyrosine kinase A6 - human >sp Q12792 Q12792 PROTEIN TYROSINE KINASE. Length = 350	gi 451482 49 Length = 350	693	95	95	95	HADCX04
192	832526	protein tyrosine kinase [Homo sapiens] >pir A55922 A55922 tyrosine kinase A6 - human >sp Q12792 Q12792 PROTEIN TYROSINE KINASE. Length = 350	gi 451482 49 Length = 350	1203	99	99	99	99	I21,AJ21
193	832575	BTG1 gene product [Homo sapiens] >gi 293306 BTG1 [Mus musculus]	gi 29509 388 Length = 350	1050	100	100	100	100	HKGAJ67
194	832576	>gi 50188 bgf [Mus musculus] >sp S20947 S20947 BTG1 protein - human >pir I48272 I48272 bgf protein - mouse >sp P31607 BTG1 HUMAN BTG1 PROTEIN (B-CELL TRANSLOCATION GENE 1 PROTEIN). Length = 350	gi 29509 388 Length = 350	1050	100	100	100	100	HKGAJ67

195	832588	mitochondrial ATP synthase subunit 9 precursor [Homo sapiens] >pir 38612 38612 ATP synthase chain 9 precursor, mitochondrial - human >sp P48201 AT93_HUMAN ATP SYNTHASE LIPID-BINDING PROTEIN P3 PRECURSOR (EC 3.6.1.34) (ATPASE PROTEIN 9) (SUBUNIT C). Length = 832634	gi 511450	2	637	85	85	H2LAD5
196	832728	immunoglobulin from VH4 family [Homo sapiens] >pir S13519 S13519 Ig heavy chain V region precursor - human	gi 37725	2	391	77	81	HCRMZ25
197	833094	>gi 553385 immunoglobulin heavy chain [Homo sapiens] {SUB 24-125} Length = 147	gi 37725	2	391	77	81	HKAIL83
198	833094	novel stromal cell protein [Mus musculus] >pir JC476 JC4761 recombinant activating gene 1 inducing protein - human >sp Q62275 Q62275 RECOMBINATION ACTIVATING PROTEIN 1 PROTEIN ACTIVATION (NOVEL STROMAL CELL PROTEIN). Length = 221	gi PID e229590	1	744	69	76	HRADC46
199	833395	(AF073957) CXC chemokine BRAK [Homo sapiens] Length = 99	gi 4140394	2	607	98	100	HHENV68
200	834326	(AF061443) G protein-coupled receptor LGR4 [Rattus norvegicus] >sp G3885470 G3885470 G PROTEIN- COUPLED RECEPTOR 1.GR4. Length = 201	gi 3885470	2	781	85	86	HWLEQ41 HE8QE56
201	834583	(AF073957) CXC chemokine BRAK [Homo sapiens] Length = 99	gi 4140394	2	607	98	100	HH-GDE66
202	834944	(AF061443) G protein-coupled receptor LGR4 [Rattus norvegicus] >sp G3885470 G3885470 G PROTEIN- COUPLED RECEPTOR 1.GR4. Length = 202	gi 3885470	2	781	85	86	HE8QE56

= 951

203	835012	(AB017169) Slit-3 protein [Homo sapiens] >sp D 036172 D1036172 SLIT-3 PROTEIN.	gnl PID d1036172	3· 344 580 1818	92 92	HCCMD55 HLHTT57
204	835104	(AB011538) MEGF5 [Homo sapiens] {SUB 785-1523} Length = 1523 (AF065389) tetraspan NET-4 [Homo sapiens] >sp O60746 O60746 TETRASPAN NET-4. Length = 268	gi 3152703	268 1080	100 100	HCROP84
205	835332	(AC002528) alpha2(I) collagen [Homo sapiens] >sp G2388555 G2388555 ALPHA2(I) COLLAGEN (FRAGMENT). Length = 1186	gi 2388555	2218 4239	100 100	HTSGZ29
206	835487					
207	836182			39 398		HFLUE31
208	836522			1819 2046		HSLFO17
209	836655			1 624		HTPCU04
210	836787	calmodulin-dependent protein kinase II-delta (EC 2.7.1.37) [Rattus norvegicus] >pir A34366 A34366 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II delta chain - rat >sp P15791 KCCD_RAT CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CII	gi 203267	767 1549	92 94	HAIED73

211	836789	GP36b glycoprotein [Homo sapiens] >pir G01447 G01447 GP36b glycoprotein - human >sp Q12907 Q12907 GP36B GLYCOPROTEIN PRECURSOR. Length = 356	gi 505652	1	849	99	99	HKAAD74
212	838577	binding protein [Oryctolagus cuniculus] >gi 182628 FK506-binding protein (FKBP) [Homo sapiens] >gi 82633 FKBP-12 Protein [Homo sapiens] >gi 182649 FK506-binding protein 12 [Homo sapiens] >gi 288196 FKBP [Homo sapiens] >gi 665650 FK-506 binding protein [H]	gi 165023	2	433	100	100	HCRQDD09
213	838717				676	900		
214	839008				2	997		
215	840063	(AF006751) ES/130 [Homo sapiens] >sp O75300 O75300 ES/130. Length = 977	gi 3299885	3	2729	84	85	HW1JIX68
216	840533				183	482		
217	840669				474	1115		
218	841140	(AF081281) lysophospholipase [Homo sapiens] >sp O75608 O75608 LYSOPHOSPHOLIPASE. Length = 230	gi 3415123	1	789	100	100	HWLLL74 HPMGM71 HAJCC51
219	841386	polypeptide GalNAc transferase-T4 [Mus musculus] >sp O08832 O08832 POLYPEPTIDE GALNAAC TRANSFERASE-T4. Length = 578	gi 2121220	491	1258	66	81	HMCCA66
220	841480				3	212		
221	841509				3	662		
222	841616				340	660		
								HDQET68 HTEL087 HWLFT95

223	841900	peptidylarginine deiminase (EC 3.5.3.15) [Rattus norvegicus] >pir A34339 DIRTR1 protein-arginine deiminase (EC 3.5.3.15) 1 - rat >sp P20717 PARD_RAT PROTEIN- ARGININE DEIMINASE (EC 3.5.3.15) (PEPTIDYLARGININE DEIMINASE). Length = 665	gi 2015960	2	439	87	90	HWLFR87
224	842054	ubiquinone-binding protein (QP) [Homo sapiens] >gi 190816 ubiquinone-binding protein precursor [Homo sapiens] >gi 37580 ubiquinone-binding protein (AA 1 - 111) [Homo sapiens] >pir A32450 A32450 ubiquinone-binding protein QP-C - human >gi 553631 ubiquinone (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus] >sp O88813 LCFE_RAT LONG- CHAIN-FATTY-ACID-COA LIGASE 5 (EC 6.2.1.3) (LONG-CHAIN ACYL- COA SYNTHETASE 5)(LACS 5). Length = 683	gi 190802	1	369	100	100	HWHPF06
225	843061	gi PID 1034547	23	2308	81	92	HDAAV92	
226	843544							HFLNB80
227	844092	(AF045573) FLI-LRR associated protein- 1 [Mus musculus] >sp O70323 O70323 FLIGHTLESS-I ASSOCIATED PROTEIN 1 (LRR DOMAIN) (FLI-LRR ASSOCIATED PROTEIN-1). Length = 628	gi 3025718	28	837	65	83	HTEKO43

228	844270	nuclear antigen EBNA-3B [Human herpesvirus 4] >pir[S2792][S2792] nuclear antigen EBNA-3B - human herpesvirus 4 >sp Q69139 Q69139 NUCLEAR ANTIGEN EBNA-3B. Length = 946	gi 330409	2	373	47	52	HWLBL06
229	844604	(AF071186) WW domain binding protein 11 [Mus musculus] >sp O88539 Q88539 WW DOMAIN BINDING PROTEIN 11. Length = 389	gi 3550082	170	2110	66	70	HNTAD40
230	844685	immunoglobulin lambda heavy chain [Homo sapiens] >gi 567132 This CDS feature is included to show the translation of the corresponding C_region. Presently translation qualifiers on C_region features are illegal [Homo sapiens] {SUB 148-177} Length = 477	gnl PID e1227585	539	1564	94	94	HASAC08
231	844855	titin [Oryctolagus cuniculus] >sp E135530 E135530 TITIN (FRAGMENT). Length = 2000	gnl PID e1355301	3	1634	34	54	HAICQ70
232	845101	(AF089814) Growth suppressor related [Homo sapiens] >sp O75956 O75956 GROWTH SUPPRESSOR RELATED. Length = 126	gi 3661529	46	627	94	94	HHESZ77
233	845141	(AB011105) KIAA0533 protein [Homo sapiens] >sp O15230 O15230 KIAA0533	gnl PID d1026389	31	966	100	100	HWMI067
234	845220	PROTEIN (LAMININ ALPHA 5 CHAIN) (FRAGMENT). >gnl PID e317479 laminin alpha 5 chain [Homo sapiens] {SUB 693-1645} Length = 1645		2	1096			HKADF64

235	845434	glutathione peroxidase [Synechocystis sp.] >pir S75885 S75885 glutathione peroxidase homolog - Synechocystis sp. (PCC 6803) >sp P74250 P74250 GLUTATHIONE PEROXIDASE (EC 1.11.1.9). Length = 169	gnl PID d1019077	3	590	50	61	HWAFl12
236	845510	dipeptidyl peptidase III [Rattus norvegicus] >sp O55096 O55096 DIPEPTIDYL PEPTIDASE (EC 3.4.14.4) (DIPEPTIDYL PEPTIDASE III) (DIPEPTIDYL AMINOPEPTIDASE III) (DIPEPTIDYL ARYLAMIDASE III) (RED CELL ANGIOTENSINASE) (ENKEPHALINASE B). Length = 827	gnl PID d1025528	3	683	96	98	HEONNN92
237	845600	procathepsin B [Homo sapiens] >pir A26498 KHH4UB cathepsin B (EC 3.4.22.1) precursor - human >sp P07858 CATB_HUMAN CATHEPSIN B PRECURSOR (EC 3.4.22.1) (CATHEPSIN B1) (APP SECRETASE). >gi 181178 lysosomal proteinase cathepsin B [Homo sapiens] {SUB 131-33}	gi 181192	223	1254	99	99	HOEME38
238	845882	(AF055666) kinesin light chain 2 [Mus musculus] >sp O88448 O88448 KINESIN LIGHT CHAIN 2. Length = 599	gi 3347848	4	1155	68	75	III.HCE82

239	846007	alpha-1-acid glycoprotein 2 [Homo sapiens] >pir JT0326 OMHU2 alpha-1-acid glycoprotein 2 precursor - human >sp P19652 A1AII HUMAN ALPHA-1-ACID GLYCOPROTEIN 2 PRECURSOR (AGP 2) (OROSOMUCOID 2)(OMD 2). >gi 388511 alpha 1-acid glycoprotein [Homo sapiens] {SU}	gi 177840	1	390	98	100	HLDBS16
240	846280	epididymal apical protein I-precursor [Macaca fascicularis] >pir S28258 S28258 androgen-regulated epididymal protein precursor - crab-eating macaque >sp Q28475 Q28475 EPIDIDYMAL APICAL PROTEIN I-PRECURSOR. Length = 776	gi 38063	31	105	36	54	HCNAK57 HASDA19
241	846286		gi 38063	203	901	36	54	HCNAK57 HASDA19
242	846388			3	1721	1721	1721	HL3AA32
243		HCRRNG17R		154	288	288	288	HCRNG17
244		HWMFG64R		1	315	315	315	HWMFG64
245		HAGCZ94R		13	102	102	102	HAGCZ94
246		HBIE174R		72	287	287	287	HBIE174
247		HUFBE67R		355	525	525	525	HUFBE67
248		HUTHM43R		2	55	55	55	HUTHM43
249		HLTGU75R		2	274	274	274	HLTGU75
250		HWLKF77R		51	134	134	134	HWLKF77
251		HWLLK67R		1	180	180	180	HWLLK67
252		HDQIE85R		3	203	203	203	HDQIE85
253		HWLFA67R		1	213	213	213	HWLFA67
254		HWLGX29R		136	351	351	351	HWLGX29
255		HWMFZ29R		324	404	404	404	HWMFZ29

265	HCDMC32R (AF014118) membrane-associated kinase [Homo sapiens] >sp O14731 O14731 MEMBRANE-ASSOCIATED KINASE. Length = 499	gi 2460023 3 272 100 100	HCDMC32
266	HCROF25R (AF034800) liprin-alpha3 [Homo sapiens] >sp G3309535 G3309535 LIPRIN-ALPHA3 (FRAGMENT). Length = 443	gi 3309535 70 381 60 65	HCROF25
267	HTEQ080R (AF035840) NADH:ubiquinone oxidoreductase B17 subunit [Homo sapiens] >sp G3800740 G3800740 NADH:UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT. Length = 128	gi 3800740 1 327 100 100	HTEQ080
268	H2LAU18R (AF035940) similar to mago nashi [Homo sapiens] >gi 2330011 (AF007862) mm-Mago [Mus musculus] >gi 2909828 (AF035939) similar to mago nashi [Mus musculus] >sp O35169 O35169 MM-MAGO. >sp G2909830 G2909830 MAGOH. >sp P50606 MGN_HUMAN MAGO NASHI PROTEIN HOMOL.	gi 2909830 2 592 100 100	H2LAU18
269	HTXP087R (AF038129) polyubiquitin [Ovis aries] >sp O46543 O46543 POLYUBIQUITIN. >gnl PID e1263307 unnamed protein product [unidentified] {SUB 77-305} >gi 63575 polyubiquitin [Bos taurus] {SUB 142-305} >gi 1762374 polyubiquitin [Gallus gallus] {SUB 1-71} >gnl PID	gi 2707837 1 330 97 97	HTXP087

270	H2LAR08R (AF040642) contains similarity to RNA recognition motifs (RNP) [Caenorhabditis elegans] >sp O44795 O44795 C50D2.5 PROTEIN Length = 200	gi 2746787	188	514	75	90	H2LAR08
271	HADAF94R (AF044957) NADH:ubiquinone oxidoreductase B15 subunit [Homo sapiens] Length = 129	gi 4164446	88	135	88	88	HADAF94
272	HEMDA91R (AF047473) testis mitotic checkpoint BUB3 [Homo sapiens] >sp O43685 O43685 TESTIS MITOTIC CHECKPOINT BUB3. Length = 326	gi 3378104	132	431	85	85	HEMDA91
273	HWMFN58R (AF051426) slow delayed rectifier channel subunit [Homo sapiens] >sp O60607 O60607 SLOW DELAYED RECTIFIER CHANNEL SUBUNIT. Length = 548	gi 2961249	3	344	100	100	HWMFN58
274	HCNDJ66R (AF034643) lambda 1 immunoglobulin light chain variable region [Homo sapiens] >gi 3023109 (AF054643) lambda 1 immunoglobulin light chain variable region [Homo sapiens] Length = 125	gi 3023109	1	276	72	73	HCNDJ66
275	HOHDH05R (AF061833) aldehyde dehydrogenase; retinal dehydrogenase; class I aldehyde dehydrogenase; ALDH-II [Xenopus laevis] >sp G3818533 G3818533 ALDEHYDE DEHYDROGENASE (EC 1.2.1.3). >pir SS1188SS1188 aldehyde dehydrogenase (NAD+) (EC 1.2.1.3); cytosolic - clawed f	gi 3818533	59	331	53	80	HOHDH05

276	HUFBP63R (AF062137) immunoglobulin heavy chain variable region [Homo sapiens] Length = 143	gi 3170737	17	463	92	96	HUFBP63
277	HUFBN90R (AF062211) immunoglobulin heavy chain variable region [Homo sapiens] Length = 149	gi 3170885	26	463	94	96	HUFBN90
278	HEBEJ57R (AF062214) immunoglobulin heavy chain variable region [Homo sapiens] Length = 142	gi 3170895	1	165	81	90	HEBEJ57
279	HDTDK65R (AF069048) immunoglobulin light chain variable region [Homo sapiens] Length = 120	gi 3328006	3	434	76	78	HDTDK65
280	HAIAD82R (AF069711) urokinase [Oryctolagus cuniculus]>sp G398274 G3982741 UROKINASE (FRAGMENT). Length = 128	gi 3982741	1	156	68	71	HAIAD82
281	HFKHD61R (AF073298) 4F5rel [Homo sapiens]>gi 3641536 (AF073297) 4F5rel [Mus musculus]>sp O75918 O75918 4F5REL..>sp O88891 O88891 4F5REL. Length = 59	gi 3641538	3	203	100	100	HFKHD61
282	H2LAX28R (AF0738817) high mobility group protein [Nannospalax ehrenbergi]>sp O88611 O88611 HIGH MOBILITY GROUP PROTEIN. Length = 215	gi 3342571	206	568	97	97	H2LAX28
283	HWLMY93R (AF078839) Rho related protein Rnd3/Rho8 [Sus scrofa]>sp O77683 O77683 RHO RELATED PROTEIN RND3/RHO8. Length = 244	gi 3386532	3	173	91	91	HWLMY93
284	HTXNL13R		3	356			HTXNL13

285	HDPWR89R (AJ005259) homologous to <i>Bombyx mori</i> multiprotein bridging factor (EMBL: AB001078) [Homo sapiens] >sp O60869 O60869 EDF-I PROTEIN. Length = 148	gn PID e1286414	1	312	79	83	HDPWR89
286	H2LAK62R	gn PID e1342961	22	165	50	76	H2LAK62
287	HWLKT15R (A1235272) UBIQUINONE/MENAQUINONE BIOSYNTHESIS	gn PID e1342961	2	301			HWLKT15
288	HATAR77R (AL021546) Cytochrome C Oxidase Polypeptide Vla-liver precursor (EC 1.9.3.1) [Homo sapiens]	gn PID e1248288	3	413	70	73	HATAR77
289	HWLWN07R (AL022237) bKL191B2.2 (BCL2-interacting killer (apoptosis-inducing) (NBK, BP4, BIP1)) [Homo sapiens] >sp E1359316 E1359316 BK1191B2.2 (BCL2-INTERACTING KILLER (APOPTOSIS-INDUCING) (NBK, BP4, BIP1)) (FRAGMENT). >gi 929655 NBK [Homo sapiens] {SUB 14-173} Le	gn PID e1359316	1	183	82	88	HWLWN07
290	HWLDI18R (AL023554) ribosomal protein [Schizosaccharomyces pombe] >sp O60118 O60118 RIBOSOMAL PROTEIN Length = 157	gn PID e1292696	3	206	43	59	HWLDI18
291	HWMEC68R		3	419			HWMEC68

292	HTXF053R	11 beta-hydroxysteroid dehydrogenase type II [Homo sapiens] >pir [38858] 38858_1 beta-hydroxysteroid dehydrogenase (EC 1.1.1.146) type 2 - human >sp P80365 DHI2_HUMAN	g 565082	3	236	88	94	HTXF053
293	HWMEMH18R	3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - human >gi 3513491 AF022380 rod photoreceptor cGMP phosphodiesterase alpha subunit [Homo sapiens] {SUB 1-122} Length = 859	pir B34611 B3461	3	203	92	92	HWMEMH18
294	HCWFF03R	5' half of the product is homologues to <i>Bacillus subtilis</i> SALCAR synthetase, 3' half corresponds to the catalytic subunit of AIR carboxylase [Homo sapiens] >pir S14147 S14147 multifunctional purine biosynthesis protein - human Length = 425	gi 28384	3	296	83	90	HCWFF03
295	HCNDP66R	A33 antigen precursor [Homo sapiens] >sp Q99795 A33_HUMAN CELL SURFACE A33 ANTIGEN PRECURSOR. Length = 319	gi 1814277	3	503	73	75	HCNDP66
296	HCRMK82R	adenosine A2b receptor [Homo sapiens] >gi 75791 A2b adenosine receptor [Homo sapiens]>pir J1229 JC1229 adenosine receptor A2b - human >sp P29275 AA2B_HUMAN	gi 178150	2	427	100	100	HCRMK82

ADENOSINE A2B RECEPTOR. Length
= 332

297	HCDAN16R alpha-1 collagen (I) [Gallus gallus] Length = 143	gi 555432	2	133	77	88	HCDAN16
298	HCEOE88R amplaxin [Homo sapiens] >pir A48063 A48063 mammary tumor/squamous cell carcinoma- associated protein EMS1 - human Length = 550	gi 182087	1	291	93	94	HCEOE88
299	HALSK30R angiogenin [Homo sapiens] >pir A90498 NRHUAG angiogenin precursor - human	gi 178250	189	416	74	76	HALSK30
300	HDRME43R anonymous [Homo sapiens] >pir 39463 39463 gene anonymous. protein - human >sp Q13769 Q13769 ANONYMOUS. Length = 147	gi 3888012	2	346	94	95	HDRME43
301	HHEFA24R APP-binding protein 1 [Rattus norvegicus] >sp G4099878 G4099878 APP-BINDING PROTEIN 1. Length = 534	gi 4099878	10	177	63	65	HHEFA24
302	HSSGC52R argininosuccinate synthetase [Bos taurus] >sp P14568 ASSY_BOVIN ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5)(CITRULLINE-- ASPARTATE LIGASE). Length = 412	gi 162697	1	438	94	95	HSSGC52

303	HCYBN49R ATP synthase beta subunit precursor [Homo sapiens] >pir A33370 A33370 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - human >sp P06576 ATPB_HUMAN ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34). >gi 28731 be	gi 179281 56 445 97	97	97	HCYBN49
304	HWMGB90R ATP synthase subunit e [Homo sapiens] >sp P56385 ATPJ_HUMAN ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34). {SUB 2-69} Length = 69	gi 2605592 1 165	58	61	HWMGB90
305	HTEAW21R ATPase coupling factor 6 subunit [Homo sapiens] >pir J0563 J0563 coupling factor 6 precursor, mitochondrial - human >sp P18859 ATPR_HUMAN ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34) (F6). Length = 108	gi 179275 47 259	93	93	HTEAW21
306	HCQCV96R ATPase subunit 6 [Homo sapiens] >sp Q34772 Q34772 ATP SYNTHASE A CHAIN (EC 3.6.1.34). Length = 226	gi PID d1007873 147	368	58	HCQCV96
307	HLTDDN74R autotaxin-1 [Homo sapiens] >sp Q13822 Q13822 AUTOTAXIN-T. >gi PID d1008938 phosphodiesterase I alpha [Homo sapiens] {SUB 1-45} Length = 863	gi 160616 2	118	85	HLTDDN74
308	HDABV61R B-creatine kinase [Gallus gallus] Length = 65	gi 211524 3	230	93	HDABV61

309	H2LAQ68R beta prime cop [Bos taurus] >pir S35312 S35312 coatomer complex beta' chain - bovine >sp P35605 COPP_BOVIN COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'- COP) (P102). {SUB 2-906} Length = 906	gi 312732	127	558	100	H2LAQ68
310	HDTLN42R beta-2-microglobulin [Pan troglodytes] >gi 177065 beta-2-microglobulin [Gorilla gorilla] >gnl PID 036168 (AB021288) beta-2-microglobulin [Homo sapiens] >pir A90976 MGHUB2 beta-2- microglobulin precursor - human >pir 36963 36963 beta-2-microglobulin pre	gi 176827	2	361	86	HDTLN42
311	HULFN47R beta-2-microglobulin [Pan troglodytes] >gi 177065 beta-2-microglobulin [Gorilla gorilla] >gnl PID 036168 (AB021288) beta-2-microglobulin [Homo sapiens] >pir A90976 MGHUB2 beta-2- microglobulin precursor - human >pir 36963 36963 beta-2-microglobulin pre	gi 176827	3	449	88	HULFN47
312	HCRM141R HWLIP53R HBAD60R HCROA35R HCROM64R HEOPS84R HKBAG82R HUTSB76R		1	528	528	HCRM141
313			2	499	499	HWLIP53
314			2	463	463	HBAA60
315			3	500	500	HCROA35
316			201	512	512	HCROM64
317			2	388	388	HEOPS84
318			32	265	265	HKBAG82
319			188	418	418	HUTSB76

320	HWLJS67R								
321	HWLLZ82R								
322	HCROM20R								
323	HDQMC24R								
324	HOCTD89R								
325	HTGAZ53R								
326	HWLKZ47R								
327	HWLLS51R								
328	HRLAJ54R								
329	HBAAD69R								
330	HWLJZ72R								
331	HWMFG06R								
332	HPRTO65R	biliary glycoprotein a [Homo sapiens]>gn PIDd1015047 biliary glycoprotein, BGPg [Homo sapiens]>gi 3172151 (AC004785) BGPg_HUMAN [Homo sapiens]>pir JH0394 JH0394 biliary glycoprotein g precursor - human Length = 417	gi 179438	2	93	97			
333	HUFDC01R	biliary glycoprotein I precursor [Homo sapiens]>gi 37198 rM1-CEA preprotein [Homo sapiens]>gi 3172148 (AC004785) BGPI_HUMAN [Homo sapiens]>pir A32164 A32164 biliary glycoprotein I precursor - human >sp P13688 BGPI_HUMAN BILARY GLYCOPROTEIN I PRECURSOR	gi 179440	108	326	87	87		
334	HWLHY44R	bone-derived growth factor [Homo sapiens]>sp Q13876 Q13876 BONE-DERIVED GROWTH FACTOR (FRAGMENT). Length = 793	gi 1203965	3	413	75	79		

335	HWLGR92R brain glycogen phosphorylase [Homo sapiens] >pir A29949 A29949 glycogen phosphorylase (EC 2.4.1.1), brain (astrocytoma cell line) - human Length = 863	gi 307200	122	238	100	100	HWLGR92
336	HCNCQ71R CAG-is1 7 [Homo sapiens] Length = 213	gi 3126984	1	93	66	77	HCNCQ71
337	HBMC128R carbonic anhydrase I (EC 4.2.1.1) [Homo sapiens] >gi 29600 carbonic anhydrase I (AA 1-261) [Homo sapiens]	gi 179793	81	293	84	84	HBMC128
	>pir JQ0786 CRHUII carbonic anhydrase (EC 4.2.1.1) I - human >sp P00915 CAH1_HUMAN CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I).{SU}						
338	HWLEN11R carbonic anhydrase I (EC 4.2.1.1) [Homo sapiens] >gi 29600 carbonic anhydrase I (AA 1-261) [Homo sapiens]	gi 179793	84	347	80	80	HWLEN11
	>pir JQ0786 CRHUII carbonic anhydrase (EC 4.2.1.1) I - human >sp P00915 CAH1_HUMAN CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I).{SU}						
339	HMSDU92R carbonic anhydrase II [Homo sapiens] >gi 179780 carbonic anhydrase II [Homo sapiens] >gi 179795 carbonic anhydrase II [Homo sapiens] >gi 29587 carbonic anhydrase II (AA 1-260) [Homo sapiens] >pir A27175 CRHUI2 carbonic anhydrase (EC 4.2.1.1) II - human	gi 179772	1	360	76	83	HMSDU92

340	HCDBF89R	carbonic anhydrase IV [Homo sapiens] >gi 409726 carbonic anhydrase IV [Homo sapiens] {SUB 73-294}; Length = 294	gi 409725	11	160	87	90	HCDBF89
341	HCNDP16R	carboxylesterase hCE-2 [Homo sapiens] >sp Q16859 Q16859	gi 407780	1	252	70	71	HCNDP16
342	HWLGX53R	CARBOXYLESTERASE (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRATE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRATE). Length = 550	gi 180223	19	138	73	73	HWLGX53
343	HWLEI156R	carinoembryonic antigen [Homo sapiens] >gi 178677 carinoembryonic antigen precursor [Homo sapiens] >pir A36319 A36319 carinoembryonic antigen precursor - human >sp P0673 ICCEM_HUMAN CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E)	gi 471077	1	453	86	87	HWLEI156
		carinoembryonic antigen [Homo sapiens] >gi 3702266 AC005797 carinoembryonic antigen CGM2 precursor - human [Homo sapiens] >pir A55811 A55811 carinoembryonic antigen CGM2 precursor - human >sp Q						

344	H2LAD26R CArG box-binding factor [Mus musculus] >gnl PID 01014884 CArG-binding factor-A [Mus musculus] >pir JQ0448 Q0448 CArG-binding factor-A - mouse >sp Q999020 CABA_MOUSE_CARG-BINDING FACTOR-A (CBF-A). Length = 285	gi 840648	43	387	98	98	H2LAD26
345	HADAF48R CD99 typeII [Homo sapiens] >sp Q00518 O00518_CD99_TYPEII. Length = 160	gi 2149135	2	151	59	59	HADAF48
346	HCRNV62R Cdc6-related protein [Homo sapiens] >gi 2465437 AF022109 HsCdc18p [Homo sapiens] >sp Q99741 Q99741 CDC6-RELATED PROTEIN. Length = 560	gi 1684903	2	442	90	91	HCRNV62
347	HCDCI17R chaperonin-like protein [Homo sapiens] >pir S48087 S48087 t-complex-type molecular chaperone CCT6 - human >gi 184462 chaperonin-like protein [Homo sapiens] {SUB 143-531} Length = 531	gi 517065	3	137	97	100	HCDCI17
348	HJUAA02R Cks1 protein homologue [Homo sapiens] >pir A36670 A36670 protein kinase cdc2 complex subunit CKS1 - human >sp P33551 CKS1_HUMAN CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (CKS-1). Length = 79	gi 29977	186	386	96	96	HJUAA02

349	IHKAKO78R	Cks1 protein homologue [Homo sapiens]>pir B36670 B36670 protein kinase cdc2 complex subunit CKS2 - human>sp P33552 CKS2_HUMAN CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 (CKS-2). Length = 79	gi 29979	2	193	77	77	IHKAKO78
350	H2CBD02R			58	522			H2CBD02
351	IHWLCSR90R	contains similarity to ATP/GTP-binding site motif (PS:PS00017) [Caenorhabditis elegans]>sp Q94180 Q94180 SIMILARITY TO ATP/GTP-BINDING SITE MOTIF. Length = 398	gi 1519671	1	351	34	60	IHWLCSR90
352	IHLAK66R	core protein II precursor [Homo sapiens]>pir A32629 A32629 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) core protein II - human Length = 453	gi 180928	126	632	79	79	IHLAK66
353	IHSDKC65R	CoxII/D-loop DNA fusion protein [Homo sapiens]>sp Q34777 Q34777 COXII/D-LOOP DNA FUSION PROTEIN (FRAGMENT). Length = 125	gi 1374867	179	346	95	97	IHSDKC65
354	IHLAK52R	CUL-2 [Homo sapiens]>sp Q13617 CUL2_HUMAN CULLIN HOMOLOG 2 (CUL-2). Length = 745	gi 1923243	24	608	100	100	IHLAK52
355	IHKAEGL2R	cyclin B1 - human>sp P14635 CGB1_HUMAN G2/MITOTIC-SPECIFIC CYCLIN B1. Length = 453	gi A32992 A32992	3	392	98	98	IHKAEGL2
356	IHKADP43R	cyclin F [Homo sapiens]>sp P41002 CG2F_HUMAN G2/MITOTIC-SPECIFIC CYCLIN F. Length = 786	gi 576781	1	375	71	71	IHKADP43

357	HLXND10R	cystatin B [Homo sapiens] >gi 235678 >spl P04080 CYTB_HUMAN CYSTATIN B (LIVER THIOL PROTEINASE INHIBITOR) (CPI-B) (STEFIN B). Length = 98	gi 291927	2	355	100	100	HLXND10
358	HUSJE17R	cytochrome c oxidase subunit II [Pan troglodytes] >spl P26457 COX2_PANPA CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1). Length = 227	gi 336514	17	208	97	98	HUSJE17
359	HLIGH82R	cytochrome c oxidase subunit Va preprotein [Mus musculus] >pir S05495 S05495 cytochrome-c oxidase (EC 1.9.3.1) chain Va precursor - mouse >spl P12787 COXA_MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR (EC 1.9.3.1). Length = 145	gi 50527	2	106	94	94	HLIGH82
360	HHBEF06R	cytochrome oxidase III [Homo sapiens] >pir A00482 OTHU3 cytochrome-c oxidase (EC 1.9.3.1) chain III - human mitochondrion (SGC1) >spl P00414 COX3_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1). >gi 245564 AF004341 cytochrome c oxidase subunit I	gi 13010	167	373	75	80	HHBEF06

361	HISCW28R	cytochrome oxidase subunit II [Homo sapiens] >gi 530071 cytochrome oxidase subunit II [Homo sapiens] >gi 530073 cytochrome oxidase subunit II [Homo sapiens] >gi 530077 cytochrome oxidase subunit II [Homo sapiens] >gi 337187 cytochrome oxidase subunit II [gi 530069	121	312	83	86	I-HISCW28
362	HODEN42R	cytochrome oxidase subunit II [Homo sapiens] >gi 530071 cytochrome oxidase subunit II [Homo sapiens] >gi 530073 cytochrome oxidase subunit II [Homo sapiens] >gi 530077 cytochrome oxidase subunit II [Homo sapiens] >gi 337187 cytochrome oxidase subunit II [gi 530069	302	469	68	71	HODEN42
363	HOEMM43R	cytochrome oxidase subunit II [Homo sapiens] >gi 530071 cytochrome oxidase subunit II [Homo sapiens] >gi 530073 cytochrome oxidase subunit II [Homo sapiens] >gi 530077 cytochrome oxidase subunit II [Homo sapiens] >gi 337187 cytochrome oxidase subunit II [gi 530069	1	180	64	67	HOEMM43
364	HPIAK29R	cytochrome oxidase subunit II [Homo sapiens] >gi 530071 cytochrome oxidase subunit II [Homo sapiens] >gi 530073 cytochrome oxidase subunit II [Homo sapiens] >gi 530077 cytochrome oxidase subunit II [Homo sapiens] >gi 337187 cytochrome oxidase subunit II [gi 530069	295	441	63	70	HPIAK29

	HUFAR71R	cytochrome oxidase subunit II [Homo sapiens] > gil S30071 cytochrome oxidase subunit II [Homo sapiens] > gil S30073 cytochrome oxidase subunit II [Homo sapiens] > gil S30077 cytochrome oxidase subunit II [Homo sapiens] > gil S337187 cytochrome oxidase subunit II [Homo sapiens] > sp Q37526 Q37526	gil S30069	128	367	82	85	HUFAR71
366	HHEUL74R	cytochrome oxidase subunit II [Homo sapiens] > sp Q37526 Q37526	gil S30075	3	227	70	74	HHEUL74
367	H2LAY36R	CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1). Length = 227	gnl PID d1010156	10	609	84	88	H2LAY36
368	H0ECI21R	cytosolic malate dehydrogenase [Homo sapiens] > gil S133269 malate dehydrogenase [Homo sapiens] > sp P40925 MDHC_HUMAN MALATE DEHYDROGENASE, CYTOPLASMIC (EC 1.1.1.37). {SUB 2-334} Length = 334	gil 81463	3	548	73	75	H0ECI21
369	HKAFY51R	decay-accelerating factor precursor [Homo sapiens] > gil 1'D d1023771 (AB003312) decay accelerating factor [Homo sapiens] {SUB 286-340}; Length = 376	gil 416178	1	429	100	100	HKAFY51
370	HMCAR63R	desmoglein 2 [Homo sapiens] > pir S38673 S38673 desmoglein 2 - human > sp Q14126 DSG2_HUMAN DESMOGLINEIN 2 PRECURSOR (HDGC). Length = 1117	gil 81478	3	335	100	100	HMCAR63
		sapiens] Length = 104						

371	HWMAN06R	dopamine- and cAMP-regulated neuronal phosphoprotein [Sus scrofa] >sp Q29277 PPD_PIG DOPAMINE- AND CAMP-REGULATED NEURONAL PHOSPHOPROTEIN (DARPP-32) (FRAGMENT). Length = 137	gi 972053	1	222	83	83	HWMAN06
372	HDPLD04R	early growth response 2 protein (EGR2) - human >gi 181987 early growth response 2 protein [Homo sapiens] {SUB 51-456} Length = 456	pir A40492 A40492	1	459	69	70	HDPLD04
373	HCEGK04R	elongation factor 2 [(Gallus gallus] >sp Q90705 EF2_CHICK ELONGATION FACTOR 2 (EF-2). {SUB 2-858} Length = 858	gi 1184958	87	182	95	95	HCEGK04
374	HWLMB57R	epidermal growth factor receptor kinase substrate [Homo sapiens] >pir 38728 38728 epidermal growth factor receptor kinase substrate - human >sp Q12929 EPS8_HUMAN EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8. Length = 822	gi 530823	1	186	93	93	HWLMB57
375	HHFHF93R	epidermal growth factor receptor precursor [Homo sapiens] >sp P21860 ERBB3_HUMAN ERBB-3 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112). >gi 1PIDe304809 unnamed protein product [Homo sapiens] {SUB 1-27} Length = 1342	gi 181980	1	180	89	89	HHFHF93

376	HCDDEM69R	epiligrin alpha 3 subunit [Homo sapiens]>pir A55347 A55347 adhesive ligand epiligrin, alpha-3 chain form A precursor - human >sp Q16787 LMA3_HUMAN LAMININ ALPHA-3 CHAIN PRECURSOR (EPILIGRIN) 170 KD SUBUNIT(E170). Length = 1713	gi 551597	136	282	95	95	HCDDEM69
377	HCHNP50R	epithelial cell marker protein 1 [Homo sapiens]>pir S38956 S38956 epithelial cell marker protein 1 - human Length = 248	gi 187302	54	218	94	94	HCHNP50
378	HAJAW27R	ERF-1 gene product [Homo sapiens]>pir S34854 S34854 epidermal growth factor-response factor 1 - human >gi 972116 ERF-1 protein [Sus scrofa] {SUB_299_337} Length = 338	gi 825653	3	488	100	100	HAJAW27
379	HAICY55R	G-rich sequence factor-1 [Homo sapiens]>gi 517196 G-rich sequence factor-1 [Homo sapiens]>sp Q12849 GRF1_HUMAN G-RICH SEQUENCE FACTOR-1(GRSF-1).>pir S48081 S48081 GRSF-1 protein - human (fragment) {SUB_94_424} Length = 424	gi 517196	3	374	50	50	HAICY55
380	HWLIA38R	gap junction protein (aa 1-283) [Homo sapiens]>pir B29005 B29005 gap junction protein Cx32 - human >sp P08034 CXB1_HUMAN GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 32)(Cx32)(GAP JUNCTION 28 KD LIVER PROTEIN). Length = 283	gi 31647	3	455	82	85	HWLIA38

381	HBXCL69R	glutamine-phenylpyruvate aminotransferase [Homo sapiens] >pir S6900 HS52790 glutamine- phenylpyruvate transaminase (EC 2.6.1.64) - human >sp Q16773 Q16773 GLUTAMINE-PIHENYL PYRUVATE AMINOTRANSFERASE (EC 2.6.1.64) (GLUTAMINE TRANSAMINASE K). Length = 422	gi 758591	81	419	61	67	HBXCL69
382	H2LAP90R	glutathione peroxidase [Homo sapiens] Length = 202	gi 488476	234	545	97	97	H2LAP90
383	HQCQR94R	glutathione peroxidase-G1 [Homo sapiens] Length = 190	gi 579930	1	114	95	95	HQCQR94
384	HTELE03R	glutathione peroxidase-G1 [Homo sapiens] Length = 190	gi 579930	14	202	100	100	HTELE03
385	HJMBN86R	glutathione-insulin transhydrogenase (216 AA) [Homo sapiens] Length = 216	gi 31746	2	202	97	100	HJMBN86
386	I-HSKJC32R	GTP:AMP phosphotransferase (EC 2.7.4.10) [Bos taurus] >gnl PID d1001680 mitochondrial adenylate kinase isozyme 3 [Bos taurus] >pir A34442 A34442 nucleoside- triphosphate--adenylate kinase (EC 2.7.4.10) 3, mitochondrial - bovine >sp P08760 KAD3_BOVIN GTP:AM	gi 163528	1	642	89	94	I-HSKJC32
387	HOEAZ62R	GTP ₋ binding protein [Sus scrofa] >sp Q29221 Q29222 GTP ₋ BINDING PROTEIN (FRAGMENT). Length = 92	gi 971836	2	100	89	92	HOEAZ62

388	HAOAG76R	guanine nucleotide-binding protein G-s-alpha-4 [Homo sapiens] >gi 31913 alpha-S1 (AA 1-380) [Homo sapiens] >pir C31927 RGHUAI GTP-binding regulatory protein Gs alpha chain (adenylate cyclase-stimulating), splice form 4 - human Length = 380	gi 386746	1	369	86	86	HAOAG76
389	HCLAD45R	guanylin [Homo sapiens] >gi 306824 guanylin [Homo sapiens] >pir A46279 A46279 guanylin precursor - human >sp Q02747 GUAN_HUMAN GUANYLIN PRECURSOR (GUANYLATE CYCLASE ACTIVATOR 2A), Length = 15 H+-ATP synthase subunit b [Homo sapiens] >pir Q1144 Q1144 H+-transporting ATP synthase (EC 3.6.1.34) chain b precursor, mitochondrial - human >sp P24539 ATPF_HUMAN ATP SYNTHASE B CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34). Length = 256	gi 183415	2	262	75	81	HCLAD45
390	H2MAC82R	heat shock protein [Homo sapiens] >pir A32319 HHLU86 heat shock protein 90-alpha - human >gi 184419 heat shock protein 86 [Homo sapiens] {SUB 1-312} >gi PID d1014121 heat shock protein 90 [Homo sapiens] {SLIB 582-732}; Length = 732	gi 509291	214	513	95	96	H2MAC82
391	H2LAJ4 R	heat shock protein [Homo sapiens] >pir A32319 HHLU86 heat shock protein 90-alpha - human >gi 184419 heat shock protein 86 [Homo sapiens] {SUB 1-312} >gi PID d1014121 heat shock protein 90 [Homo sapiens] {SLIB 582-732}; Length = 732	gi 703087	75	632	98	98	H2LAJ4I
392	HWLGH40R	H[KL]I [Homo sapiens] >sp O60765 O60765 H[KL]I. Length = 605	gnl PID d1026110	1	597	92	93	HWLGH40

393	HBJFH33R	HLA DP4 beta-chain [Homo sapiens]>gi 296648 pot. hla-dp-beta 1 [Homo sapiens]>pir A02229 [HLA]HUPB MHC class II histocompatibility antigen HLA-DP beta 1 chain (allele DPB4.1) precursor - human>sp P04440 [B2P_HUMAN HLA CLASS II HISTOCOMPATIBILITY ANTIGEN]	gi 306858	97	369	88	92	HBJFH33
394	HISDV92R	homeobox c1 protein [Homo sapiens]>sp Q64081 Q64081 HOX-B HOX-2 {CLONE 17A}. {SLUB 137-196} Length = 217	gi 306878	51	404	72	72	HISDV92
395	HMQCG89R	Hox5.4 gene product (AA 1-95) [Homo sapiens]>pir B32830 [B32830 homeotic protein Hox D8 - human (fragment)>sp P13378 [HXD8_HUMAN HOMEBOX PROTEIN HOX-D8 (HOX-4E)(HOX-5.4)(FRAGMENT). Length = 95	gi 32400	158 1	388 345	100 100	100 100	HMQCG89 HE9QB35
397	HDABQ50R	hsOrc2p [Homo sapiens]>sp Q13416 [ORC2_HUMAN ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2. Length = 577	gi 113107	204	368	91	91	HDABQ50

398	HNT EG83R	hydroxymethylglutaryl-CoA lyase [Homo sapiens] >pir A45470 A45470 hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) - human >sp P35914 HMGL_HUMAN HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (EC 4.1.3.4) (HMG-COA LYASE)(HL) (3-HYDROXY-3-METHYLGLUTARATE-COA LYASE	gi 184503	2	391	83	83	HNT EG83
399	HFVHM90R	hydroxymethylglutaryl-CoA synthase [Homo sapiens] >gi 2463646 3-hydroxy-3-methylglutaryl CoA synthase [Homo sapiens] >pir S71623 S71623 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) precursor, mitochondrial - human >sp P54868 HMCM_HUMAN HYDROXYMETHYLGLU	gi 619877	2	319	92	94	IHFVHM90
400	HOSNF90R	hypothetical 18K protein (rRNA)- goldfish mitochondrion (SGC1) Length = 166	pir JC1348 JC1348	257	340	59	62	I-HOSNF90
401	HSDJE56R	hypothetical 18K protein (rRNA)- goldfish mitochondrion (SGC1) Length = 166	pir JC1348 JC1348	2	70	67	73	HSDJE56
402	IWLGC87R	hypothetical protein 2 (rRNA external transcribed spacer) - mouse Length = 153	pir S12206 S12206	1	135	96	96	IWLGC87

403	HTPAC28R	I-plastin [Homo sapiens] >pir A56536 A56536 plastin, intestine-specific - human >sp Q14651 PLSL_HUMAN I-PLASTIN (INTESTINE-SPECIFIC PLASTIN). Length = 629	gi 405230	68	325	92	93	HTPAC28
404	IMCGGN07R	ICK=INTRON-CONTAINING KALLIKREIN {ALTERNATIVELY SPLICED, INTRON 2}; Length = 216	sp G998972 C998972	1	498	98	99	IMCGGN07
405	HFIBV16R	Id1 gene product [Homo sapiens] >pir S47524 S47524 gene Id1 protein - human Length = 154	gi 457785	2	238	89	89	HFIBV16
406	HBMTT01R	Ig alpha-2 chain C region (allootype A2m(1))-human >sp P01877 ALC2_HUMAN Ig ALPHA-2 CHAIN C REGION. >gi 184761 Ig alpha-2 H-chain constant region (aa at 166) [Homo sapiens] {SUB 2-340} Length = 340	pir B22360 B22360	2	154	80	80	HBMTT01
407	HBVMVM66R	Ig gamma chain C region - chimpanzee >gnl P D e40518 C1-2 domain of IgG [Pan troglodytes] {SUB 12-134} >gnl P D e40517 CH3 domain of IgG [Pan troglodytes] {SUB 135-234} Length = 234	pir PT0207 PT0207	148	435	70	77	HBVMVM66
408	HABGC21R	Ig heavy chain (DOI) - human (fragment)>gnl P D e4381 reading frame CH1 [Homo sapiens] {SUB 121-218} Length = 241	pir S69131 S69131	1	228	50	56	HABGC21
409	HWL.GE72R	Ig kappa light chain (VJ) [Homo sapiens] >pir S40343 S40343 Ig kappa chain V-J region - human Length = 128	gi 441375	11	421	75	79	HWL.GE72

410	HLJBX69R	IgM B-cell receptor associated protein (BAP) 37 [Mus musculus] >pir S46996 S46996 B-cell receptor-associated protein BAP37 - mouse >sp Q61336 Q61336 BCR-ASSOCIATED PROTEIN 37 (IGM B-CELL RECEPTOR ASSOCIATED PROTEIN 37) (BAP). Length = 298	gi 541734	1	279	100	100	HLJBX69
411	HWAFW14R	immunoglobulin I from VH4 family [Homo sapiens] >pir S13519 S13519 Ig heavy chain V region precursor - human >gi 553385 immunoglobulin heavy chain [Homo sapiens] {SUB 24-125} Length = 147	gi 37725	2	139	94	100	HWAFW14
412	HWAFK04R	immunoglobulin heavy chain [Homo sapiens] >pir E36005 E36005 Ig heavy chain V region (M72) - human {SUB 36-157} Length = 157	gi 567126	48	473	78	86	HWAFK04
413	HEPNA09R	immunoglobulin heavy chain [Homo sapiens] >pir G36005 G36005 Ig heavy chain V region (M74) - human {SUB 38-158} Length = 158	gi 567127	3	206	81	87	HEPNA09
414	HCRQD03R	immunoglobulin heavy chain [Homo sapiens] Length = 152	gi 567128	1	573	76	82	HCRQD03
415	HAPSK08R	immunoglobulin heavy chain variable region [Homo sapiens] >gi 903667 Ig heavy chain variable region VH [Homo sapiens] {SUB 1-97} >gi 976311 This CDS feature is included to show the translation of the corresponding V_segment. Presently translation qualifie	gi 1791017	1	363	79	81	HAPSK08

416	HBMTS1R	immunoglobulin IgH heavy chain Fd fragment [Homo sapiens] Length = 221	gi 468237	1	375	68	70	HBMTS1
417	HCNDR62R	immunoglobulin kappa light chain [Homo sapiens] >pir A37927 A37927 Ig kappa chain C region (allootype Igv(1.2)) - human (fragment) {SUB 138-236}; Length = 236	gnl PID e224083	245	337	100	100	HCNDR62
418	HNJBF13R	immunoglobulin lambda light chain gene product [Homo sapiens] >pir S25738 S25738 Ig lambda chain - human Length = 231	gi 33702	3	308	90	93	HNJBF13
419	HLYCD69R	immunoglobulin lambda light chain gene product [Homo sapiens] >pir S25743 S25743 Ig lambda chain - human (fragment) Length = 145	gi 33712	2	481	86	89	HLYCD69
420	HWAFK89R	immunoglobulin lambda light chain gene product [Homo sapiens] >pir S25750 S25750 Ig lambda chain - human Length = 235	gi 33730	2	460	87	92	HWAFK89
421	HWCAA53R	immunoglobulin light chain variable region [Homo sapiens] >gi 3142470 (AF063703) immunoglobulin lambda light chain variable region [Homo sapiens] {SUB 20-127} >gi 575243 immunoglobulin lambda chain precursor [Homo sapiens] {SUB 26-127} >gi 1PID d 020826 V immunoglobulin light chain variable region [Homo sapiens] Length = 154	gi 465170	1	342	74	88	HWCAA53
422	HYAAAY47R		gi 465168	2	292	70	74	HYAAAY47
423	HMCJF14R			21	596			HMCJF14
424	HE8QU88R			13	141			HE8QU88

425	HFVGPII R	L-FABP [Homo sapiens] >pir A22280 FZHU_L_fatty acid-binding protein, hepatic - human >sp P07148 FABL_HUMAN FATTY ACID-BINDING PROTEIN, LIVER (L-FABP). Length = 127	gi 182358	29	322	98	98	HFVGPII
426	HWLQH07R	Irp gene product [Homo sapiens]	gi 895840	3	554			
427	HSIGN24R	>pir S57723 S57723_Irp protein - human >sp Q14764 MVP_HUMAN MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN). Length = 896	gi 895840	2	250	89	93	HWLQH07 HSIGN24
428	HWLKH07R	lysophosphatidic acid acyltransferase-beta [Homo sapiens] Length = 278	gi 2155240	74	298	96	97	HWLKH07
429	HAPQC14R	macrophage capping protein [Homo sapiens] >pir A43358 A43358 >sp P40121 CAPG_HUMAN MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATOR PROTEIN CAP-G). >gi 515505 Cap-G [Homo sapiens] {SUB I-172} Length = 348	gi 187456	2	538	96	98	HAPQC14
430	HSODB48R	malonyl-CoA decarboxylase (EC 4.1.1.9) pir A33313 A33313 >goose >gi 305323 malonyl CoA decarboxylase [Anser anser] {SUB 33-462} Length = 462 Length = 385	3	32	466	77	81	HSODB48
431	HBEACT5R	membrane glycoprotein [Homo sapiens] Length = 385	gi 307132	2	217	73	79	HBEACT5
432	HBGMJ24R	mitochondrial RNA polymerase [Homo sapiens] Length = 1230	gi 2114396	3	479	100	100	HBGMJ24

433	HBJEN94R	mitotic kinase-like protein-1 [Homo sapiens] >pir S28262 S28262 kinesin-related protein MKLP-1 - human >sp Q02241 MKL_P_HUMAN MITOTIC KINESIN-LIKE PROTEIN-1. Length = 960	gi 34672	1	327	89	89	HBJEN94
434	HCLAE73R	motor protein [Homo sapiens] 1.length = 721	gi P1D d1005183	73	324	100	100	HCLAE73
435	HCNDN88R	mucin 2 precursor, intestinal - human (fragments) >gi 86396 mucin [Homo sapiens] {SUB 626-1895} >gi 86398 MUC2 [Homo sapiens] {SUB 2037-3020} >gi 88874 intestinal mucin [Homo sapiens] {SUB 1916-2193} >gi 88615 mucin-like protein [Homo sapiens] {SUB 23	pir A49963 A4393	1	171	95	97	HCNDN88
436	HSIDX70R	N-benzoyl-L-tyrosyl-p-amino-benzoic acid hydrolase alpha subunit [Homo sapiens] >pir S60193 HYHUMA meprin A (EC 3.4.24.18) alpha chain precursor - human >sp Q16819 MEPA_HUMAN MEPRIN A ALPHA-SUBUNIT PRECURSOR (EC 3.4.24.18) (ENDOPEPTIDASE-2) (N- BENZOYL-L-	gi 525475	2	253	94	94	HSIDX70

437	HL.WBC39R	Na+/H+ exchanger NHE-1 isoform [human, heart, Peptide, 815 aa] [Homo sapiens]>pir 57487 57487 Na+/H+-exchanging protein NHE-1 - human >spl P19634 NAH1_HUMAN SODIUM/HYDROGEN EXCHANGER (Na(+)/H(+)) EXCHANGER 1) (NHE-1) (Na+/H+ ANTIPORTER, AMILORIDE-SENSI	bbs 143522	2	388	77	77	HL.WBC39
438	HWLAA06R	NADH-dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - chimpanzee mitochondrion (SGC1) (fragment) >spl P03906 NU4M_PANT_NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENT). Length = 152	pir A00435 A0043	5	66	194	86	97 HWLAA06
439	HASCH25R	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-39KD)(CI-39KD). >spl 89049 NADH dehydrogenase (ubiquinone) [Homo sapiens] {SUB 3-377} Length = 377	sp Q16795 NUEM_HUMAN	57	143	78	82	HASCH25
440	HL.QGB87R	NADPH-ferritinoprotein reductase (EC 1.6.2.4) - human >spl P16435 NCPR_HUMAN NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR). {SUB 2-677} Length = 677	pir A3342 A6055	7	1	411	92	93 HLQGB87

441	IIIDMD17R	neutrophil gelatinase associated lipocalin [Homo sapiens]	gi 929657	1	621	74	78	IIIDMD17
		>sp P80188 NGAL_HUMAN NEUTROPHIL GELATINASE- ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (25 kD ALPHA-2-MICROGLOBULIN- RELATED SUBUNIT OF MMP-9) (LIPOCALIN-2) (ONCOGENE 24P3). Length = 198						
442	HAOAC69R	nuclear autoantigen [Homo sapiens] >pir A3724 A37244 nuclear autoantigen Sp-100 - human Length = 480	gi 178689	3	209	88	88	HAOAC69
443	IHWLEQ08R	Nuclear localization signal at AA 569- 573, 576-580, 579-583; acidic transcr. activ. domain 620-640.; homeobox motif 653-676 [Homo sapiens] >pir A47456 A47456 down-regulated in adenoma (DRA) - human >sp P40879 DRA_HUMAN DRA PROTEIN (DOWN-REGULATED IN ADENO	gi 291964	191	364	75	84	IHWLEQ08
444	HKAAV70R	nucleic acid binding protein [Homo sapiens] >pir 38191 I38191 nucleic acid binding protein - human (fragment) >sp Q15410 Q15410 NUCLEIC ACID BINDING PROTEIN (FRAGMENT). Length = 163	gi 431953	1	432	73	73	HKAAV70

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445	I-OCTB64R	ORIGINAL PIGR [unidentified] >gi 456346 Polymeric immunoglobulin receptor [Homo sapiens] >bbs 62408 transmembrane secretory component, poly-Ig receptor, SC [human, colonic adenocarcinoma cell line, Peptide, 764 aa] [Homo sapiens] >bbs 113253	gnl P1D e307278	3	212	85	90	I-OCTB64
446	HOFNB62R	ornithine decarboxylase [Bos taurus]>gi 63449 ornithine decarboxylase [Bos taurus] >sp P27117 DCOR_BOVIN ORNITHINE DECARBOXYLASE (EC 4.1.1.17) (ODC), >gi 604513 ornithine decarboxylase [Bos taurus] {SUB 1-34} Length = 461	gi 1036793	1	312	85	90	HOFNB62
447	HAUAU04R	p22 phagocyte b-cytochrome [Homo sapiens] >pir A28201 A28201 cytochrome b-245 alpha chain - human >sp P13498 C24A_HUMAN CYTOCHROME B-245 LIGTH CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEUTROPHIL CYTOCHROME B, 22 KD POLYPEPTIDE) (P22-PHOX) (CYTOCHROME B(558) AL	gi 189106	1	267	87	88	HAUAU04
448	HNFJE41R	p47-phox [Homo sapiens] >sp O43842 O43842 p47-PHOX. Length = 390	gi 2754713	1	423	94	97	HNFJE41
449	IICIOH92R	phosphoprotein phosphatase (EC 3.1.3.16) catalytic beta chain - pig (fragment) Length = 293	pir B27430 B27430	2	88	93	93	IICIOH92
450	HOUID53R	phosphorylation regulatory protein HP-10 pir A61382 A61382 human Length = 492	85	213	45	49	HOUID53	

451	HCRMW41R	polypeptide BM28 [Homo sapiens] Length = 892	gi 468704	1	282	100	100	HCRMW41
452	HOVAX78R	porin [Homo sapiens] >pir A45972 A45972 mitochondrial porin, long form - human >sp P45880 POR2_HUMAN VOLTAGE-DEPENDENT ANION- SELECTIVE CHANNEL PROTEIN 2 (VDAC2) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN). >gi 90201 porin [Homo sapiens] {SUB 27-347; Len	gi 90200	2	214	94	98	HOVAX78
453	HWAEH57R	precursor [Homo sapiens] >sp P06314 KV4C_HUMAN IG KAPPA CHAIN PRECURSOR V-I V REGION (B17). Length = 134	gi 37910	1	462	91	93	HWAEH57
454	HHBH76R	presenilin 1-463 [Homo sapiens] >pir S63683 S63683 presenilin 1-463 - human Length = 463	gi 1244638	1	303	98	98	HHBH76
455	HBJFA18R	prosomeal p27K protein [Homo sapiens] >gnl PID 1002062 proteasome subunit R-IOTA [Rattus sp.]>pir S30274 S30274 multicatalytic endopeptidase complex (EC 3.4.99.46) iota chain - human >pir JX0230 JX0230 multicatalytic endopeptidase complex (EC 3.4.99.46)	gi 35682	178	402	79	83	HBJFA18
456	HCRNF16R	protein kinase [Homo sapiens] >sp P51956 NEK3_HUMAN SERINE/THREONINE-PROTEIN KINASE NEK3 (EC 2.7.1.-) (NIMA- RELATED PROTEIN KINASE 3) (HSPK 36) (FRAGMENT). Length = 459	gi 479173	336	473	73	79	HCRNF16

457	HAHEK76R	putative surface glycoprotein [Homo sapiens] >sp PS380 C211_HUMAN PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR (C21ORF3). Length = 180	gn PID e18811	33	440	83	86	HAHEK76
458	HEOPT38R	>gill302662 renin-binding protein [Homo sapiens] >pirjX0188 JX0188 renin-binding protein - human Length = 417	gn PID d1001551	2	316	100	100	HEOPT38
459	HOSCG81R	ribonucleoprotein La [Homo sapiens] >sp Q15367 Q15367 RIBONUCLEOPROTEIN (La) (FRAGMENT). >gi 338496 SS-B/La protein [Homo sapiens] {SUB 121-171} Length = 355	gi 337457	1	297	96	96	HOSCG81
460	HTFMD43R	ribosomal protein L39 [Homo sapiens] >gnl PID d101213 ribosomal protein L39 [Homo sapiens] >gi 575382 ribosomal protein L39 [Rattus norvegicus] >pir JC4229 R6RT139 ribosomal protein L39 - rat >pir G02654 G02654 ribosomal protein L39 - human Length = 51	gi 3373419	3	242	100	100	HTFMD43
461	HDTGQ68R	ribosomal protein L7a large subunit [Homo sapiens] >gi 34203 L7a protein [Homo sapiens] >gi 35512 PL-A-X polypeptide [Homo sapiens] >gi 36647 ribosomal protein L7a [Homo sapiens] >gi 56956 ribosomal protein L7a (AA 1- 266) [Rattus rattus] >pir S1971 R5HU7A	gi 337495	43	291	100	100	HDTGQ68

462	H2LAR73R	ribosomal protein S15a [Rattus norvegicus] >pir JC2234 JC2234 ribosomal protein S15a - rat Length = 130	gi 495273	23	505	100	100	H2LAR73
463	HAMFM26R	ribosomal protein S6 kinase 1 [Homo sapiens] >pir S1901 S1901 ribosomal protein S6 kinase 2 - human >sp Q15418 KS61_HUMAN RIBOSOMAL PROTEIN S6 KINASE II ALP1(A 1 (EC 2.7.1.-) (S6K1I-ALPHA 1)(P90-RSK 1)(RIBOSOMAL S6 KINASE 1)(RSK1)(PP90RSK1). Length =	gi 292457	3	458	97	97	HAMFM26
464	HBMTM61R	Rieske Fe-S protein [Homo sapiens] Length = 274	gi 488299	1	219	53	55	HBMTM61
465	I1W1IPK71R	RIP [Homo sapiens] >pir J38992 J38992 receptor interacting protein RIP - human (fragment) Length = 372	gi 829617	198	320	56	64	I1W1IPK71
466	IHWBBJ39R	Sec23 protein [Homo sapiens] Length = 767 selenium donor protein [Homo sapiens] Length = 383	gnl PID e236014	2	127	81	84	IHWBBJ39
467	IHSLJJ36R		gi 1000284	2	319	96	98	IHSLJJ36
468	IHSODD94R	settnoprotein P [Homo sapiens] Length = 381	gnl PID e1192260	2	232	61	70	IHSODD94
469	IHMIA25R	serine kinase [Homo sapiens] >pir S45337 S45337 serine protein kinase SRPK1 - human >sp Q12890 Q12890 SERINE KINASE. Length = 655	gi 507213	1	330	82	82	IHMIA25
470	IHWLEM94R	serine protease [Homo sapiens]. Length = 492	gi 2507613	2	304	78	82	IHWLEM94

471	HCNDW17R	Sm protein G [Homo sapiens] >pir S55054 S55054 Sm protein G - human >spi Q15357 Q15357 SM PROTEIN G. Length = 76	gi 806566	1	240	100	100	HCNDW17
472	HWLEY08R	SNAP23A protein [Homo sapiens] >gnl P1D e1331767 (A1011915) synaptosome associated protein of 23 kilodaltons, isoform A [Homo sapiens] >pir JC5296 C5296 vesicle-membrane fusion protein SNAP-23A - human >sp O00161 O00161 VESICLE- MEMBRANE FUSION PROTEIN SN	gnl P1D e290695	222	608	97	97	HWLEY08
473	HULFN68R	sorcin CP-22 [Homo sapiens] >gi 459836 >gnl S52094 S52094 sorcin - human >gi 2772536 (AC003991) calcium binding protein amplified in multidrug- resistant cells [Homo sapiens] {SUB 1- 68} Length = 198	gi 338482	2	409	88	91	HULFN68
474	HMEJD77R	SRp30c [Homo sapiens] >gnl P1D e1248292 (A1021546) pre- mRNA splicing factor SRp30c [Homo sapiens] >gi 4099429 splicing factor SRp30c [Homo sapiens] >pir S559075 S559075 splicing factor SRp30c - human >sp G4099429 G4099429 SPLICING FACTOR SRP30C. Length = 22 stimulator of TAR RNA binding [Homo sapiens] Length = 539	gi 1049078	3	263	46	48	HMEJD77
475	HS2AD15R		gi 1200184	1	336	87	88	HS2AD15

476	HTEJ32R	STM-7 [Homo sapiens] >sp Q92749 Q92749 TYPE I PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE BETA (EC 2.7.1.68) (STM-7 PROTEIN).	gn PID e206448	3	341	100	100	HTEJJ32
477	HETTIF46R	>g 1743883 type I phosphatidylinositol- 4-phosphate 5-kinase beta [Homo sapiens] {SUB 112-502} >g 1743879 type I phosphatidylinosi- sulfate transporter [Homo sapiens] >sp P50443 DTD_HUMAN SULFATE TRANSPORTER (DIASTROPHIC DYSPLASIA PROTEIN). Length = 739 thrombospondin 2 [Homo sapiens] >pir A47379 TSI1UP2 thrombospondin 2 precursor - human Length = 1172 thymosin beta-4 precursor [Rattus norvegicus] >pir S2084 S2084 thymosin beta-4 precursor - rat (fragment) >g 339689 thymosin beta-4 [Homo sapiens] {SUB 13-56} >pir A01521 TNBOB4 thymosin beta-4 - bovine {SUB 14-56} >g 825683 open reading frame [Homo s- tissue-specific secretory protein [unidentified] >g 32051 HE4 protein [Homo sapiens] >pir S25454 S25454 HE4 protein - human >sp Q14508 EP4_HUMAN MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR (HE4) (EPIDIDYMAL SECRETORY PROTEIN E4). Length =	g 549988	1	228	71	71	HETTIF46
478	H2CBS58R	g 307506	3	455	96	97	97	H2CBS58
479	H2LAB77R	g 207318	98	265	100	100	100	H2LAB77
480	H2OAJ23R	g 583141	2	223	62	62	62	H2OAJ23

481	HWAFP88R	TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3). Length = 204	sp Q64152 BTF3_MOUSE	85	471	92	93	HWAFP88
482	HDTH151R	transcription factor-like protein 4 - human Length = 298	pir JC5333 JC5333	2	565	82	86	HDTH151
483	HWMER67R	tryptase-III [Homo sapiens] >sp Q15664 Q15664 TRYPTASE-III (FRAGMENT). Length = 267	gi 339985	21	218	92	92	HWMER67
484	HTXOU93R	tumor susceptibility protein [Homo sapiens]>sp Q99816 Q99816 TUMOR. SUSCEPTIBILITY PROTEIN. Length = 390	gi 3184258	2	439	100	100	HTXOU93
485	HANKB37R	ubiquitin [Plasmodium falciparum] >sp Q26029 Q26029 UBIQUITIN. Length = 77	gi 552237	11	115	70	73	HANKB37
486	HWLHN38R	ubiquitin-conjugating enzyme [Mus musculus]>sp O88738 O88738 UBIQUITIN-CONJUGATING ENZYME. Length = 4845	gn P1Dle 311091	129	347	77	83	HWLHN38

487	HOSDZ35R	UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase [Homo sapiens] >spQ14435	gn PID e20971	2	286	85	85	HOSDZ35
		POLYPEPTIDE N-ACETYLGLALACTOSAMINYLTRANSFERASE (EC 2.4.1.4) (PROTEIN-UDP ACETYLGLALACTOSAMINYLTRANSFERASE) (UDR-PERASE) (UDR-GALNAC:POLYPEPTIDE N-ACETYLGLALACTOSAMINYLTRANSFERASE)						
488	HKMMA52R	UDP-glucuronosyltransferase [Homo sapiens] >pir[A3]340 A31340	gi 624725	3	284	98	98	HKMMA52
		glucuronosyltransferase (EC 2.4.1.17) UGTA1 precursor - human >sp G245274 G245274 PHENOLTRANSFERASE=UGT1I1 PRODUCT. {SUB I-286} >gi 264549 (AF014112) phenol UDP-glucuronosyltransferase [Homo						
489	H2LAB37R			93	290			
490	H2LAP46R			206	568			
491	H6BSE61R			67	369			
492	H6EEE76R			149	277			
493	H6EEV26R			2	88			
494	HABAFF88R			40	216			
495	HABGD41R			1	147			
496	HACBS75R			5	187			
497	HACCA48R			5	91			
498	HACCS19R			3	341			
499	HADAB25R			1	261			
500	HAGGL96R			3	347			

501	HAGGT37R	3	113
502	HAHDR66R	27	347
503	HAJCC53R	164	418
504	HAJCL80R	3	122
505	HANKF43R	372	566
506	HAPCM11R	69	152
507	HAPNT66R	1	66
508	HAQAG47R	2	148
509	HAQBW58R	3	260
510	HAQMHH45R	91	363
511	HAQMI94R	1	183
512	HARNC74R	84	272
513	HATBA87R	98	202
514	HATBG77R	174	392
515	HBAGQ79R	1	231
516	HBCAN64R	2	82
517	HBGCA44R	1	123
518	HBGFX27R	3	281
519	HBGMU38R	40	429
520	HBJB010R	1	93
521	HBJCC53R	2	106
522	HBJED55R	1	252
523	HBJGR39R	2	106
524	HBJLU30R	39	344
525	HBKEC78R	93	245
526	HBMST81R	1	192
527	HBMTJS1R	150	323
528	HBMWTF72R		
529	HBWBD78R	1	111
530	HBXCU02R	2	226
531	HCDAK65R	2	79
		1	138

532	HCDBM08R	130	339
533	HCDCP10R	72	206
534	HCDDQ63R	3	116
535	HCEEH05R	204	380
536	HCEIQ92R	1	90
537	HCFCD01R	28	228
538	HCFCR43R	64	360
539	HCFLT83R	3	104
540	HCHA092R	193	342
541	HCHOH49R	183	344
542	HCHPG05R	365	616
543	HCIAD24R	98	301
544	HCNCA90R	380	532
545	HCNCN80R	120	353
546	HCNCY51R	184	267
547	HCNCY63R	1	81
548	HCND071R	1	213
549	HCNDV83R	64	303
550	HCNUB26R	119	289
551	HCQBN22R	2	94
552	HCQCL27R	116	235
553	HCQCL48R	57	251
554	HCQCL96R	287	430
555	HCQDC74R	145	360
556	HCQDH94R	20	76
557	HCQDJ42R	149	388
558	HCMD77R	3	185
559	HCROME02R	3	293
560	HCRRMX88R	3	284
561	HCRRNA70R	40	204
562	HCRRNP66R	3	431

563	HCRNX32R	2	196
564	HCR0H25R	3	128
565	HCR0J05R	66	170
566	HCR0J68R	3	239
567	HCR0K68R	2	208
568	HCR0K94R	1	210
569	HCR0M30R	3	365
570	HCR0Q34R	29	136
571	HCR0Q54R	3	98
572	HCR0Z66R	239	427
573	HCRPC61R	3	194
574	HCRPG28R	95	229
575	HCRPL80R	59	235
576	HCRPN52R	3	191
577	HCRPS40R	208	321
578	HCRPV74R	179	409
579	HCRQC89R	2	85
580	HCWDS78R	322	558
581	HDCAA21R	1	120
582	HDDAA85R	139	258
583	HDPGO03R	110	352
584	HDPLB08R	142	360
585	HDQDB15R	220	417
586	HDQEX80R	274	492
587	HDRMI91R	3	116
588	HDTJO85R	36	197
589	HDTMJ22R	192	608
590	HE6CS28R	40	213
591	HE6DJ45R	2	64
592	HE7TJ40R	62	268
593	HE9FH12R	182	307

594	H-HE9HJ57R	3	74
595	H-HE9QH08R	360	596
596	H-HE9TC50R	198	425
597	H-HEAAL59R	1	150
598	H-HECAR32R	448	675
599	H-HECAR85R	361	534
600	H-HELFE05R	32	187
601	H-HEMF188R	25	343
602	H-HEMFR18R	83	397
603	H-HEONL43R	2	76
604	H-HE SAC53R	3	116
605	H-HE TJB05R	1	138
606	H-HE TJC36R	1	102
607	H-HE ADM62R	1	78
608	H-HE FATE31R	2	361
609	H-HE ATZ30R	3	152
610	H-HE CEL77R	3	278
611	H-HE FBN43R	174	491
612	H-HE GAF10R	272	469
613	H-HE ECOIR	1	144
614	H-HE IR75R	317	427
615	H-HE IUB90R	2	124
616	H-HE IUM71R	37	159
617	H-HE OXL53R	1	117
618	H-HE PBO66R	196	408
619	H-HE TB157R	47	220
620	H-HE TCC22R	1	126
621	H-HE XGX46R	1	114
622	H-HE GAME72R	2	199
623	H-HE BCSS3R	142	279
624	H-HE BHP81R	87	221

625	HGCCOX03R	323	511	
626	HHBES92R	349	483	
627	HHBEW72R	13	219	
628	HHERT59R	2	88	
629	HHMMD64R	31	252	
630	HHSGT13R	428	619	
631	HISED82R	1	126	
632	HHMAH76R	2	253	
633	HJMAN56R	1	180	
634	HJMA054R	1	291	
635	HKDAD56R	2	109	
636	HKLSD93R	89	298	
637	HLMFH16R	1	447	
638	HLQBD52R	1	195	
639	HLQCQ73R	3	350	
640	HLQEF47R	348	503	
641	HLQFMS0R	136	291	
642	HLQFY61R	411	575	
643	HLQGA76R	210	404	
644	HLQGE53R	1	66	
645	HLTEV09R	210	371	
646	HLXNE63R	142	258	
647	HLXTF64R	2	136	
648	HMACF85R	23	430	
649	HMAIA15R	108	452	
650	HMCHZ07R	247	402	
651	HMCISS4R	84	242	
652	HMSFW88R			
653	HMSMW71R	1	69	
654	HNHMR05R	290	514	
655	HNJBB78R	77	598	
		91	282	

656	HNTMA96R	3	362
657	HINTRL32R	130	291
658	HNTST76R	2	397
659	HCNC55R	67	156
660	HCND06R	147	275
661	HCND49R	133	273
662	HODEH30R	2	154
663	HODFA26R	263	550
664	HODHL89R	106	279
665	HOEJM67R	2	364
666	HOGBN48R	147	380
667	HOHCX95R	2	364
668	HORB43R	3	365
669	HOIHN53R	235	345
670	HOIJE10R	72	254
671	HPBEE63R	107	211
672	HPEBO20R	1	237
673	HPJBE91R	1	312
674	HPTRW82R	32	133
675	HPWDC51R	33	272
676	HPWDK52R	1	330
677	HRDBJ82R	2	334
678	HRDH93R	2	121
679	HS2AD53R	1	120
680	HSATR92R	3	203
681	HSdzG83R	5	136
682	HSICQ60R	2	118
683	HSIF-A64R	3	449
684	HSKNN36R	108	527
685	HSKY52R	2	124
686	HSLJA55R	2	169

687	HSODA95R	2	169
688	HSPBS19R	1	372
689	HSSGK43R	3	155
690	HSXFJ91R	3	242
691	HTEMB57R	168	410
692	HTGBR05R	37	138
693	HTLGA72R	3	455
694	HTLIX61R	1	102
695	HTNTF25R	307	426
696	HTWCP79R	91	180
697	HTXFA64R	3	263
698	HUSIF91R	218	412
699	HUSIN48R	259	462
700	HUSIX68R	98	493
701	HUSZN23R	36	131
702	HTSD20R	104	256
703	HWAC110R	66	275
704	HWAF163R	3	272
705	HWAGZ89R	176	385
706	HWBAQ20R	1	177
707	HWBHHM83R	2	298
708	HWLAC24R	11	133
709	HWLAC81R	64	360
710	HWLBFB27R	3	149
711	HWLBS90R	195	347
712	HWLCU10R	55	120
713	HWLEH13R	2	379
714	HWLE67R	375	527
715	HWLEM49R	244	354
716	HWLFPP27R	2	79
717	HWLGCG20R	92	208

718	HWLGK22R	209	373
719	HWLGM21R	244	354
720	HWLGP37R	8	181
721	HWLGS46R	40	324
722	HWLGU40R	2	202
723	HWLGX65R	3	230
724	HWLHD09R	2	310
725	HWLHD50R	3	98
726	HWLHM40R	2	208
727	HWLHW89R	56	382
728	HWLID17R	64	276
729	HWLJM20R	3	158
730	HWLJA26R	34	135
731	HWLJA28R	1	108
732	HWLJG57R	240	404
733	HWLJL19R	119	292
734	HWLJPS0R	1	147
735	HWLKG82R	1	360
736	HWLKG95R	1	300
737	HWLK153R	1	144
738	HWLKM09R	2	100
739	HWLKM86R	44	226
740	HWLKM95R	2	184
741	HWLKU25R	3	137
742	HWLQS83R	1	117
743	HWLQU65R	361	558
744	HWLRL59R	1	225
745	HWLRP86R	2	253
746	HWLRO49R	3	158
747	HWLUF60R	84	218
748	HWLUI37R	51	263

749	HWLUR41R				33	155
750	HWLVD60R				1	174
751	HWLVV50R				1	72
752	HWMAN61R				3	107
753	HWMEB47R				87	185
754	HWMEH13R				2	256
755	HWMEH26R				168	341
756	HWMEL50R				131	400
757	HWMFB31R				100	285
758	HWMFL66R				61	153
759	HWMFO93R				2	79
760	HWMFP01R				120	284
761	HZAAD81R				1	144
762	HWLHN70R				2	160
763	HFIXX57R				2	211
	URF 3 (NADH dehydrogenase subunit) [Homo sapiens] >gi 506832 protein_3	gi 13011				
	[Homo sapiens] >pir A00422 DNHUN3					
	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - human mitochondrion (SGCI) >sp P03897 NU3M_HUMAN					
	NADH-UBIQUINONE					
	OXIDOREDUCTASE CHAIN 3 (EC 1.6					
764	HMAFE48R					
	UFR 3 (NADH dehydrogenase subunit) [Homo sapiens] >gi 506832 protein_3	gi 13011	47	205	90	100
	[Homo sapiens] >pir A00422 DNHUN3					
	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - human mitochondrion (SGCI) >sp P03897 NU3M_HUMAN					
	NADH-UBIQUINONE					
	OXIDOREDUCTASE CHAIN 3 (EC 1.6					

765	HRODJ88R	URF 3 (NADH dehydrogenase subunit) [Homo sapiens] >gi 506832 protein 3 [Homo sapiens] >pir A00422 DNHUN3 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - human mitochondrion (SGC1) >sp P03897 NU3M_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6	gi 13011	55	213	83	94	HRODJ88
766	HWLAR31R	URF 3 (NADH dehydrogenase subunit) [Homo sapiens] >gi 506832 protein 3 [Homo sapiens] >pir A00422 DNHUN3 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - human mitochondrion (SGC1) >sp P03897 NU3M_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6	gi 13011	56	214	91	100	HWLAR31
767	HNLHLH26R	v-SNARE [Cricetulus griseus] >sp Q08522 O08522 v-SNARE. Length = 250	gi 1912453	73	243	64	76	HNLHLH26
768	H2LAU24R	weakly similar to gastrula zinc finger protein [Caenorhabditis elegans] >sp Q09998 Q09998 PUTATIVE 55.5 KD ZINC FINGER PROTEIN R144.3 IN CHROMOSOME III. Length = 492	gi 746495	78	488	45	60	H2LAU24
769	HATDR94R	X box binding protein-1 [Homo sapiens] >pir A36299 A36299 transcription factor hXBp-1 - human Length = 260	gi 306893	2	367	95	100	HATDR94
770	HWLLI185R	X-linked deafness dystonia protein [Homo sapiens] >sp Q60220 O60220 X- LINKED DEAFNESS DYSTONIA PROTEIN. Length = 97	gi 3123843	410	580	60	80	HWLLI185

771	HBBHM67R	XP-C repair complementing protein (p58/HHR23B) [Homo sapiens] >pir S44346 S44346 RAID23 protein homolog - human Length = 409	gnl PID d1005181	3	191	96	96	HBBHM67
772	HSYCH4 R	yeast methionyl-tRNA synthetase homolog [Homo sapiens] >pir JC5224 JC5224 methionine-tRNA ligase (EC 6.1.1.10) - human >gil 804996 mitoxantrone-resistance associated gene [Homo sapiens] {SUB 423-900} Length = 900	gnl PID e218477	2	373	90	90	HSYCH4
773	HWLJRS3R	zinc finger protein PZF [Mus musculus] >pir l48724 l48724 zinc finger protein PZF - mouse >sp Q62511 Q62511 ZINC FINGER PROTEIN PZF. Length = 455	gil 453376	1	552	81	83	HWLJRS3

ID NO:774 through SEQ ID NO:1546) are sufficiently accurate and otherwise suitable for a

(where Y may be any of the polypeptide sequences disclosed in the sequence listing as SEQ

sequence listing as SEQ ID NO:1 through SEQ ID NO:773) and the translated SEQ ID NO:Y

SEQ ID NO:X (where X may be any of the polynucleotide sequences disclosed in the

more of any one or more of these public ESTs are optionally excluded from the invention.

Table 3 indicates public ESTs, of which at least one, two, three, four, five, ten, or

herein.

is not full-length, a full-length cDNA can be obtained by methods described elsewhere

however, the clone is believed to encode a full-length polypeptide. In the case where a clone

described in the sequence listing or the clone may have less. In the vast majority of cases,

directly sequencing the referenced clone. The reference clone may have more sequence than

sequence of the assembled conting and at least a portion of SEQ ID NO:X was determined by

contig sequence. This clone ID references the cDNA clone which contains at least the 5' most

contig sequence. The ninth column of Table 1 provides a unique "Clone ID" for a clone related to each

transliteration product of SEQ ID NO:X and the database sequence.

"Similarity" (percent similarity) observed between the aligned sequence segments of the

therefore. The seventh and eighth columns provide the "% Identity" (percent identity) and "%

Also provided are polynucleotides encoding such proteins and the complementary strand

by the portion of SEQ ID NO:X delineated by the nucleotide position nos. "Start" and "End".

Invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded

the preferred ORF shown in the sequence listing as SEQ ID NO:Y. In one embodiment, the

the contig), "Start" and "End", in the polynucleotide sequence "SEQ ID NO:X" that delineate

The fifth and sixth columns in Table 1 provide the location (nucleotide position nos. within

1, "Overlap," provides the database accession no. for the database sequence having similarity.

unrelated to any sequences previously described in the literature. The fourth column, in Table 1 are

such as GenBank (NCBI). The great majority of the cDNA sequences reported in Table 1 are

transliteration product to an amino acid sequence found in a publicly accessible gene database,

Name." provides a putative identification of the gene based on the sequence similarity of its

for each column and/or column cancer associated sequence. The third column in Table 1, "Gene

The second column in Table 1, provides a unique "Sequence/Contig ID" identification

cancer antigen polynucleotide sequences of the invention.

The first column of Table 1 shows the "SEQ ID NO:" for each of the 773 column

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, but also a sample of plasmid DNA containing the related cDNA clone as SEQ ID NO:Y, but also a sample of plasmid DNA containing the related cDNA clone deposited with the ATCC, as set forth in Table I). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.

The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneous insertion or deletion of nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 15

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 Variet y of uses well known in the art and described further below. For instance, SEQ ID NO:X has uses including, but not limited to, in designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the related cDNA clone contained in a library deposited with the ATCC. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y have uses that include, but are not limited to, generating antibodies which bind specifically to the colon cancer polypeptides, or fragments thereof. and/or to the colon cancer antigen polyptides encoded by the cDNA clones identified in Table 1.

15 skilled in the art to complete the sequence of the DNA included in a clone isolatable from the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one coding region of a human gene. Although the sequence listing lists only a portion of the region of a human gene or in other cases such clone may include a substantial portion of the ATCC Deposits by use of a sequence listed as SEQ ID NO:X may include the entire coding SEQ ID NO:X described in Table 1 (column 9). Thus, a clone which is isolatable from the material includes the DNA clones which were partially sequenced and are related to the 10 and the vector in which the DNA is contained is also indicated in Table 5. The deposited "the deposits" herein. The tissues from which the clones were derived are listed in Table 5, a plasmid vector or a phage vector, as shown in Table 5. These deposits are referred to as each is a mixture of DNA clones derived from a variety of human tissue and cloned in either

ATCC Deposits	Deposit Date	ATCC Designation Number	
LPO1, LPO2, LPO3, LPO4,	May-20-97	209059, 209060, 209061, 209062.	LPO5, LPO6, LPO7, LPO8,
LPO9, LPO10, LPI1,		209063, 209064, 209065, 209066,	209067, 209068, 209069
LPI13	Jan-12-98	209578	
LPI14	Jul-16-98	203067	
LPI15	Jul-16-98	203068	
LPI16	Feb-1-99	203609	
LPI17	Feb-1-99	203610	
LPI20	Nov-17-98	203485	
LPI21	Jun-18-99	PTA-252	
LPI22	Jun-18-99	PTA-253	
LPI23	Dec-22-99	PTA-1081	

5 Table 2

The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC sequences, as well as the use of the DNA sequences. The material deposited with the ATCC

on:

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. 10 Mees, M. A. et al., *Strategies* 5:58-61 (1992)) are commercially available from Stratagene. Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. PBS contains ampicillin resistance gene and PBK contains a neomycin resistance gene. Phagemid PBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into *E. coli* strain XL-1 Blue, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focusing Vectors* PCR[®] 2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 15:59 (1993). Vector lambda BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector PCR[®] 2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 20 DH10B, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nucleic Acids Res.* 25 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nucleic Acids Res.* 9677-9686 (1988) and Mead, D. et al., *BioTechnology* 9: (1991).

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the cDNA contained in a deposited cDNA clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include, but are not limited to, preparing probes or primers from the sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

herewith further described, and others apparent to those skilled in the art.

Also provided in Table 5 is the name of the vector which contains the cDNA clone.

Each vector is routinely used in the art. The following additional information is provided for

ATCC Deposits by use of a sequence (or portion thereof) listed in Table 1 by procedures

included in column 3 of Table 3. In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula; it is just a representative example.

Table 3.

Sequence/ Contig ID	General formula	Genbank Accession No.
500802	Prefeably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula where a is any integer between 1 to 619 of SEQ ID NO:1, b is an integer of 1 to 633, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:1, and where b is greater than or equal to a + 14. or equal to a + 14.	
531091	Prefeably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula where a is any integer between 1 to 281 of SEQ ID NO:2, b is an integer of 1 to 295, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:2, and where b is greater than or equal to a + 14.	
533147	Prefeably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula where a is any integer between 1 to 428 of SEQ ID NO:3, b is an integer of 1 to 442, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:3, and where b is greater than or equal to a + 14.	
558860	Prefeably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula where a is any integer between 1 to 740 of SEQ ID NO:4, b is an integer of 1 to 754, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:4, and where b is greater than or equal to a + 14.	
561730	Prefeably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula where a is any integer between 1 to 379 of SEQ ID NO:5, b is an integer of 1 to 393, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:5, and where b is greater than or equal to a + 14.	
585938	Prefeably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula where a is any integer between 1 to 525 of SEQ ID NO:6, b is an integer of 1 to 539, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:6, and where b is greater than or equal to a + 14.	
587783	Prefeably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula where a is any integer between 1 to 790 of SEQ ID NO:7, b is an integer of 1 to 804, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:7, and where b is greater than or equal to a + 14.	

666316	Preferably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer of 1 to 1994 of SEQ ID D and b is an integer of 1 to 2008, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:15, and where b is greater than or equal to a + 14.
669229	Preferably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 749 of SEQ ID D and b is an integer of 1 to 763, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:17, and where b is greater than or equal to a + 14.
670471	Preferably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 1912 of SEQ ID D and b is an integer of 1 to 1926, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:18, and where b is greater than or equal to a + 14.
676611	Preferably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 2287 of SEQ ID D and b is an integer of 1 to 2301, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:19, and where b is greater than or equal to a + 14.
691240	Preferably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 524 of SEQ ID D and b is an integer of 1 to 538, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:20, and where b is greater than or equal to a + 14.
702977	Preferably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 1389 of SEQ ID D and b corresponds to the positions of nucleotide residues shown in SEQ ID NO:21, and where b is greater than or equal to a + 14.

	residues shown in SEQ ID NO:21, and where b is greater than or equal to a + 14.	709517
	where a is any integer between 1 to 478, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where b is greater than or equal to a + 14.	714730
	one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1238 of SEQ ID NO:23, b is an integer of 15 to 1252, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:23, and where b is greater than or equal to a + 14.	714834
	one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1060 of SEQ ID NO:24, b is an integer of 15 to 1074, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:24, and where b is greater than or equal to a + 14.	715016
	one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1172 of SEQ ID NO:25, b is an integer of 15 to 1186, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:25, and where b is greater than or equal to a + 14.	719584
	one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 874 of SEQ ID NO:26, b is an integer of 15 to 888, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:26, and where b is greater than or equal to a + 14.	724637
	one or more poly nucleotides comprising-a-nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 775 of SEQ ID NO:27, b is an integer of 15 to 789, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:27, and where b is greater than or equal to a + 14.	728392

738716	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	Or equal to a + 14.
739056	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	Or equal to a + 14.
739143	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	Or equal to a + 14.
742329	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	Or equal to a + 14.
742557	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	Or equal to a + 14.
745481	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	Or equal to a + 14.
746035	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	Or greater than or equal to a + 14.

753731	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 370 of SEQ ID No.:36, b is any integer of 15 to 384, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID No.:36, and where b is greater than or equal to a + 14.
754383	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 468, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID No.:37, and where b is greater than or equal to a + 14.
756749	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1095 of SEQ ID No.:38, b is an integer of 15 to 1095, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID No.:38, and where b is greater than or equal to a + 14.
757980	Preferrably excluded from the present invention are R38216, R63249, R78721, HO1441, H02537, H02640, H86258, H86321, N21599, W16868, W31882, W56228, AA058568, AA100609, AA115890 where a is any integer between 1 to 1751 of SEQ ID No.:39, b is any integer of 15 to 1751, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID No.:39, and where b is greater than or equal to a + 14.
764818	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1945, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID No.:40, and where b is greater than or equal to a + 14.
765140	Preferrably excluded from the present invention are R69702, R76994, R77002, HO1357 where a is any integer between 1 to 588, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID No.:41, and where b is greater than or equal to a + 14.
766893	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1568, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID No.:42, and where b is greater than or equal to a + 14.
771338	Preferrably excluded from the present invention are PCT/US00/05883 WO 00/55351

		One or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	771412
		where a is any integer between 1 to 1060, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:43, and where b is greater than or equal to a + 14.	772226
		One or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	773057
	N41723	where a is any integer of 15 to 892, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:45, and where b is greater than or equal to a + 14.	773173
		One or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	780154
		where a is any integer between 1 to 1215 of SEQ ID NO:47, b is an integer of 15 to 1229, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:47, and where b is greater than or equal to a + 14.	780768
		One or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	780779
		where a is any integer between 1 to 1671 of SEQ ID NO:49, b is an integer of 15 to 1685, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:48, and where b is greater than or equal to a + 14.	

		Sequence described by the general formula of a-b.	shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.
782394	Preferrably excluded from the present invention are R24689, R25853, R34457, R66839, R68536, H22874, H45555, N50184, AA015963, AA028939, AA028938	Sequence described by the general formula of a-b. where a is any integer between 1 to 660, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.	where a is any integer between 1 to 646 of SEQ ID NO:50, b is an integer of 15 to 660, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.
782395	Preferrably excluded from the present invention are R24689, R25853, R34457, R66839, R68536, H22874, H45555, N50184, AA015963, AA028939, AA028938	Sequence described by the general formula of a-b. where a is any integer between 1 to 660, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.	where a is any integer between 1 to 646 of SEQ ID NO:50, b is an integer of 15 to 660, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.
783160	Preferrably excluded from the present invention are R24689, R25853, R34457, R66839, R68536, H22874, H45555, N50184, AA015963, AA028939, AA028938	Sequence described by the general formula of a-b. where a is any integer between 1 to 660, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and where b is greater than or equal to a + 14.	where a is any integer between 1 to 642 of SEQ ID NO:52, b is an integer of 15 to 635, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and where b is greater than or equal to a + 14.
783506	Preferrably excluded from the present invention are R24689, R25853, R34457, R66839, R68536, H22874, H45555, N50184, AA015963, AA028939, AA028938	Sequence described by the general formula of a-b. where a is any integer between 1 to 660, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:34, and where b is greater than or equal to a + 14.	where a is any integer between 1 to 644 of SEQ ID NO:54, b is an integer of 15 to 378, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:34, and where b is greater than or equal to a + 14.
784446	Preferrably excluded from the present invention are R24689, R25853, R34457, R66839, R68536, H22874, H45555, N50184, AA015963, AA028939, AA028938	Sequence described by the general formula of a-b. where a is any integer between 1 to 660, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:364 of SEQ ID NO:53, and where b is greater than or equal to a + 14.	where a is any integer between 1 to 1353 of SEQ ID NO:53, b is an integer of 15 to 1367, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:364 of SEQ ID NO:53, and where b is greater than or equal to a + 14.
784832	Preferrably excluded from the present invention are R24689, R25853, R34457, R66839, R68536, H22874, H45555, N50184, AA015963, AA028939, AA028938	Sequence described by the general formula of a-b. where a is any integer between 1 to 660, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:682 of SEQ ID NO:55, and where b is greater than or equal to a + 14.	where a is any integer between 1 to 1058, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:682 of SEQ ID NO:55, and where b is greater than or equal to a + 14.
786813	W44740, AA235981	Preferrably excluded from the present invention are R24689, R25853, R34457, R66839, R68536, H22874, H45555, N50184, AA015963, AA028939, AA028938	Preferrably excluded from the present invention are R24689, R25853, R34457, R66839, R68536, H22874, H45555, N50184, AA015963, AA028939, AA028938
792139		One or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	One or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.

		where a is any integer between 1 to 630 of SEQ ID NO:57. b is an integer of 15 to 644, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:57. And where b is greater than or equal to a + 14.
793987	Prefeably excluded from the present invention are sequence described by the general formula of a-b, where a is any integer between 1 to 766, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:58. And where b is greater than or equal to a + 14.	
805715	Prefeably excluded from the present invention are sequence described by the general formula of a-b, where a is any integer between 1 to 2361, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:59. And where b is greater than or equal to a + 14.	
811111	Prefeably excluded from the present invention are sequence described by the general formula of a-b, where a is any integer between 1 to 4002, N46020, W92748, N22686, N25829, N27270, N31401, N40002, N46020, W92748, N292871. And where a is any integer between 1 to 1472, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:60. And where b is greater than or equal to a + 14.	
811113	Prefeably excluded from the present invention are sequence described by the general formula of a-b, where a is any integer between 1 to 1658 of SEQ ID NO:61. And where b is an integer of 15 to 1672, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:61. And where b is greater than or equal to a + 14.	
823902	Prefeably excluded from the present invention are sequence described by the general formula of a-b, where a is any integer between 1 to 1540, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:62. And where b is an integer of 15 to 1561, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:62. And where b is greater than or equal to a + 14.	
826518	Prefeably excluded from the present invention are sequence described by the general formula of a-b, where a is any integer between 1 to 1030 of SEQ ID NO:63. And where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:63, and where b is an integer of 15 to 1044, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:63, and where b is greater than or equal to a + 14.	
826704	Prefeably excluded from the present invention are sequence described by the general formula of a-b, where a is any integer between 1 to 837 of SEQ ID NO:64. And where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:64, and where b is an integer of 15 to 848, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:64, and where b is greater than or equal to a + 14.	

827720	PREFERABLY EXCLUDED FROM THE PRESENT INVENTION ARE ONE OR MORE POLYNUCLEOTIDES COMPATIMING A NUCLEOTIDE SEQUENCE DESCRIBED BY THE GENERAL FORMULA OF A-B, WHERE A IS ANY INTEGER BETWEEN 1 TO 2779 OF SEQ ID NO:65, B IS AN INTEGER OF 15 TO 2793, WHERE BOTH A AND B CORRESPOND TO THE POSITIONS OF NUCLEOTIDE RESIDUES SHOWN IN SEQ ID NO:65, AND WHERE B IS GREATER THAN OR EQUAL TO A + 14.	
828102	PREFERABLY EXCLUDED FROM THE PRESENT INVENTION ARE ONE OR MORE POLYNUCLEOTIDES COMPATIMING A NUCLEOTIDE SEQUENCE DESCRIBED BY THE GENERAL FORMULA OF A-B, WHERE A IS ANY INTEGER BETWEEN 1 TO 289 OF SEQ ID NO:66, B IS AN INTEGER OF 15 TO 303, WHERE BOTH A AND B CORRESPOND TO THE POSITIONS OF NUCLEOTIDE RESIDUES SHOWN IN SEQ ID NO:66, AND WHERE B IS GREATER THAN OR EQUAL TO A + 14.	
828180	PREFERABLY EXCLUDED FROM THE PRESENT INVENTION ARE ONE OR MORE POLYNUCLEOTIDES COMPATIMING A NUCLEOTIDE SEQUENCE DESCRIBED BY THE GENERAL FORMULA OF A-B, WHERE A IS ANY INTEGER BETWEEN 1 TO 1396 OF SEQ ID NO:67, B IS AN INTEGER OF 15 TO 1410, WHERE BOTH A AND B CORRESPOND TO THE POSITIONS OF NUCLEOTIDE RESIDUES SHOWN IN SEQ ID NO:67, AND WHERE B IS GREATER THAN OR EQUAL TO A + 14.	
828386	PREFERABLY EXCLUDED FROM THE PRESENT INVENTION ARE ONE OR MORE POLYNUCLEOTIDES COMPATIMING A NUCLEOTIDE SEQUENCE DESCRIBED BY THE GENERAL FORMULA OF A-B, WHERE A IS ANY INTEGER BETWEEN 1 TO 1010 OF SEQ ID NO:68, B IS AN INTEGER OF 15 TO 1848, WHERE BOTH A AND B CORRESPOND TO THE POSITIONS OF NUCLEOTIDE RESIDUES SHOWN IN SEQ ID NO:68, AND WHERE B IS GREATER THAN OR EQUAL TO A + 14.	
828658	PREFERABLY EXCLUDED FROM THE PRESENT INVENTION ARE ONE OR MORE POLYNUCLEOTIDES COMPATIMING A NUCLEOTIDE SEQUENCE DESCRIBED BY THE GENERAL FORMULA OF A-B, WHERE A IS ANY INTEGER BETWEEN 1 TO 184, WHERE BOTH A AND B CORRESPOND TO THE POSITIONS OF NUCLEOTIDE RESIDUES SHOWN IN SEQ ID NO:69, AND WHERE B IS GREATER THAN OR EQUAL TO A + 14.	
828919	PREFERABLY EXCLUDED FROM THE PRESENT INVENTION ARE T6671, T6672, T71638, R08935, R09044, R09373, T80114, T85695, R00758, R00759, R12645, R19577, R20545, R22041, R22097, R20545, R59701, R59811, R60034, R60096, R60694, R76255, R81371, R81370, H04390, R83679, H71735, H72298, H47647, H0415, H05912, H47622, H47647, N35542, N49731, N52660, N67681, N75596, W03490, A0164628, A0215698, A0233182, A0233196, A0236759, A0256822, A0429489.	

829572	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. T63032 AA428534	where a is any integer between 1 to 398 of SEQ ID NO:71, b is an integer of 15 to 412, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:71, and where b is greater than or equal to a + 14.
830138	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. R01611, N76461, W74577, W79757.	where a is any integer between 1 to 1347 of SEQ ID NO:72, b is an integer of 15 to 1361, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:72, and where b is greater than or equal to a + 14.
830208	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. R01611, N76461, W74577, W79757.	where a is any integer between 1 to 914 of SEQ ID NO:73, b is an integer of 15 to 928, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:73, and where b is greater than or equal to a + 14.
830248	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. AA045350, AA056064, AA1190524	where a is any integer between 1 to 1172 of SEQ ID NO:74, b is an integer of 15 to 1186, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:74, and where b is greater than or equal to a + 14.
830275	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. T90376, R46154, R46154, A4224239.	where a is any integer between 1 to 919 of SEQ ID NO:75, b is an integer of 15 to 933, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:75, and where b is greater than or equal to a + 14.
830286	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. AA467906, AA483293, AA502593.	where a is any integer between 1 to 1950 of SEQ ID NO:76, b is an integer of 15 to 1964, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:76, and where b is greater than or equal to a + 14.
830347	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. AA513313, AA594453, AA594570.	where a is any integer between 1 to 1788 of SEQ ID NO:77, b is an integer of 15 to 1802, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:77, and where b is greater than or equal to a + 14.

830348	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 981 of SEQ ID NO:78, b is an integer of 15 to 995, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:78, and where b is greater than or equal to a + 14.	A.A983601
830364	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 1201 of SEQ ID NO:79, b is an integer of 15 to 1215, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:79, and where b is greater than or equal to a + 14.	
830394	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 2646 of SEQ ID NO:80, b is an integer of 15 to 2660, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:80, and where b is greater than or equal to a + 14.	
830412	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 1776 of SEQ ID NO:82, b is an integer of 15 to 1350, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:82, and where b is greater than or equal to a + 14.	
830436	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 1746, b is an integer of 15 to 1491, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:83, and where b is greater than or equal to a + 14.	R63785, H21426, N55384, AA009460.
830464	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 1477 of SEQ ID NO:84, b is an integer of 15 to 1491, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:84, and where b is greater than or equal to a + 14.	H06247, H19227, W52470
830471	Preferrably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 1491, b is an integer of 15 to 1491, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:84, and where b is greater than or equal to a + 14.	R28064, R28282, A.A143044, A.A151127.

			Sequence described by the general formula of a-b.
830564	Prefeably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	AA95857, N88876 AA934427, AA962214, AA995455. AA877207, AA878505, AA923685. AA743161, AA834774, AA872783. AA480672, AA587251, AA576938. AA173985, AA186698, AA188326. AA160087, AA160675, AA173629. AA129593, AA129330, AA128581. AA100913, AA100912, AA129619. AA031697, AA031863, AA058529. W72566, W76560, AA011078, AA011079, H93354, W4215, W42513, W61060. H07926, H29767, H29768, H38826. R13392, R40908, R40908, H02114, T60268, T61648, T68371, T88743, R00503.	One or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.
830542	Prefeably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	NO:90.-b-is an integer between 1 to 2018 of SEQ ID where a is any integer between 1 to 2018 of SEQ ID where b corresponds to the positions of nucleotide residues shown in SEQ ID NO:90, and where b is greater than or equal to a + 14.	
830548	Prefeably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	NO:89.-b-is an integer of 15 to 1925 of SEQ ID where a is any integer between 1 to 1925 of SEQ ID where b corresponds to the positions of nucleotide residues shown in SEQ ID NO:89, and where b is greater than or equal to a + 14.	
830528	Prefeably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	NO:88.-b-is an integer of 15 to 1163, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:88, and where b is greater than or equal to a + 14.	
830509	Prefeably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	NO:87.-b-is an integer of 15 to 2230, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:87, and where b is greater than or equal to a + 14.	
830500	Prefeably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	NO:86.-b-is an integer between 1 to 3068, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:86, and where b is greater than or equal to a + 14.	
830477	Prefeably excluded from the present invention are one or more poly nucleotides comprising a nucleotide sequence described by the general formula of a-b.	W74073, W79680, AA021098, AA179389, AA182649, AA188175, AA191449, AA228943, AA228942, AA594459, AA737972, C02737	
			Sequence described by the general formula of a-b.
			where a is any integer between 1 to 954 of SEQ ID where b corresponds to the positions of nucleotide residues shown in SEQ ID NO:85, and where b is greater than or equal to a + 14.

	where a is any integer between 1 to 1774 of SEQ ID NO:91, b is an integer of 15 to 1788, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:91, and where b is greater than or equal to a + 14.	
830611	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 481 of SEQ ID NO:92, b is an integer of 15 to 495, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:92, and where b is greater than or equal to a + 14.	
830618	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1363 of SEQ ID NO:93, b is an integer of 15 to 1377, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:93, and where b is greater than or equal to a + 14.	R43709. R43709. H09113. H43746. N92632. AA022453. AA120876. AA120889. AA493651. AA493785. AA494347. AA565392. AA743179. AA769161
830620	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2805 of SEQ ID NO:94, b is an integer of 15 to 2819, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:94, and where b is greater than or equal to a + 14.	
830630	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 691 of SEQ ID NO:95, b is an integer of 15 to 705, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:95, and where b is greater than or equal to a + 14.	
830654	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3458 of SEQ ID NO:96, b is an integer of 15 to 3472, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:96, and where b is greater than or equal to a + 14.	
830660	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1202 of SEQ ID NO:97, b is an integer of 15 to 1216, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:97, and where b is greater than or equal to a + 14.	
830661	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1172 of SEQ ID	

	NO:98. b is an integer of 15 to 1186, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:98, and where b is greater than or equal to a + 14.	
830704	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1106 of SEQ ID NO:99, b is an integer of 15 to 1120, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:99, and where b is greater than or equal to a + 14.	
830765	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1211 of SEQ ID NO:100, b is an integer of 15 to 1225, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:100, and where b is greater than or equal to a + 14.	
830778	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1199 of SEQ ID NO:101, b is an integer of 15 to 1213, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:101, and where b is greater than or equal to a + 14.	
830784	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1550 of SEQ ID NO:102, b is an integer of 15 to 1564, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:102, and where b is greater than or equal to a + 14.	R63323, R66534, AA491630
830800	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1443 of SEQ ID NO:103, b is an integer of 15 to 1457, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:103, and where b is greater than or equal to a + 14.	
830821	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 771 of SEQ ID NO:104, b is an integer of 15 to 785, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:104, and where b is greater than or equal to a + 14.	
830849	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 907 of SEQ ID NO:105, b is an integer of 15 to 921, where both a	AA258128, AA259034, AA262104, AA742612, AA804402

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:105, and where b is greater than or equal to a + 14.	
830903	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 578 of SEQ ID NO:106, b is an integer of 15 to 592, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:106, and where b is greater than or equal to a + 14.	
830913	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2234 of SEQ ID NO:107, b is an integer of 15 to 2248, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:107, and where b is greater than or equal to a + 14.	R06463, R06517, R48006, R51455, R61502, R72398, R72399, R74489, R74599, H07933, H08039, H61149, H62056, H90758, H90809, N32837, N42283, W40284, W45325, AA079353, AA079592, AA100814, AA102342, AA111844, AA122150, AA134127, AA134128, AA148738, AA148709, AA164240, AA164899, AA164275, AA171881, AA179310, AA179453, AA180811, AA180955, AA187432, AA190377, AA190791, AA190383, AA458475, AA427428, AA468548, AA554518, AA595768, AA595893, AA640601, AA574035, AA658143, AA863401, AA906604, AA995159, C03746, C04875, C05396, AA033510
830920	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 771 of SEQ ID NO:108, b is an integer of 15 to 785, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:108, and where b is greater than or equal to a + 14.	
830938	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 597 of SEQ ID NO:109, b is an integer of 15 to 611, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:109, and where b is greater than or equal to a + 14.	AA053612
830980	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 650 of SEQ ID NO:110, b is an integer of 15 to 664, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:110, and where b is greater than or equal to a + 14.	
831014	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4051 of SEQ ID NO:111, b is an integer of 15 to 4065, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:111, and where b is greater than or equal to a + 14.	
831026	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1478 of SEQ ID NO:112, b is an integer of 15 to 1492, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:112, and where b is greater than or equal to a + 14.	
831031	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1468 of SEQ ID NO:113, b is an integer of 15 to 1482, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:113, and where b is greater than or equal to a + 14.	R46004, R46004, H06850, N27532, N30567, N30842, N34647, N40349, N41369, N49777, N52708, N62958, W68355, W68490, AA054602, AA193410, AA193648, AA503204, AA688236, AA730103, AA736540, AA747555, AA811522, AA863169, N79861
831055	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3717 of SEQ ID NO:114, b is an integer of 15 to 3731, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:114, and where b is greater than or equal to a + 14.	
831057	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1301 of SEQ ID NO:115, b is an integer of 15 to 1315, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:115, and where b is greater than or equal to a + 14.	R69415, R69546, H14127, H62767, N62927, N63320, W00649, W01189, AA053293, AA058396, AA149075, AA458528, AA418699, AA418770, AA505598, AA576507, AA730033, AA805864, AA988279, AA991217, D82661, C21298
831062	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1306 of SEQ ID NO:116, b is an integer of 15 to 1320, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:116, and where b is greater than or equal to a + 14.	
831117	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2011 of SEQ ID NO:117, b is an integer of 15 to 2025, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:117, and where b is greater than or equal to a + 14.	R80585, R80586, N49020, AA173625, AA173981, AA557142, AA627866, AA847195, A1015673
831122	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1281 of SEQ ID NO:118, b is an integer of 15 to 1295, where both a and b correspond to the positions of nucleotide	R72079, R72128, AA715820, AA804163, AA809123, AA641490

	residues shown in SEQ ID NO:118, and where b is greater than or equal to a + 14.	
831125	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1243 of SEQ ID NO:119, b is an integer of 15 to 1257, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:119, and where b is greater than or equal to a + 14.	N80647, AA114140, AA143553, AA156386, N68188, AA070867
831132	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 383 of SEQ ID NO:120, b is an integer of 15 to 397, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:120, and where b is greater than or equal to a + 14.	
831152	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 862 of SEQ ID NO:121, b is an integer of 15 to 876, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:121, and where b is greater than or equal to a + 14.	AA765155
831157	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1264 of SEQ ID NO:122, b is an integer of 15 to 1278, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:122, and where b is greater than or equal to a + 14.	T57943, R34275, R35472, R77406, R77405, N23203, N59015, AA160841, AA610280, AA857624, AI089936, AI094724, AI094954
831160	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3101 of SEQ ID NO:123, b is an integer of 15 to 3115, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:123, and where b is greater than or equal to a + 14.	
831193	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 365 of SEQ ID NO:124, b is an integer of 15 to 379, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:124, and where b is greater than or equal to a + 14.	
831197	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1253 of SEQ ID NO:125, b is an integer of 15 to 1267, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:125, and where b is	AA134613

	greater than or equal to a + 14.	
831217	Preferrably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 827 of SEQ ID NO:126, b is an integer of 15 to 841, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:126, and where b is greater than or equal to a + 14.	
831239	Preferrably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1158 of SEQ ID NO:127, b is an integer of 15 to 1172, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:127, and where b is greater than or equal to a + 14.	T68487, T88923, T88994, R09550, R09663, R26714, R26937, H27046, H28228, H30272, H30335, N27966, N36884, N46156, N93575, W21407, W44513, W44514, W47626, W47627, W56215, W60528, W80465, W80574, W92729, AA002237, AA002076, AA099290, AA099291, AA127753, AA127706, AA128275, AA128572, AA148737, AA149497, AA419078, AA423819, AA506117, AA534694, AA552105, AA552219, AA583468, AA622094, AA633205, AA878663, AA911544, AA916173, AA974873, AA988860, AI056396, AI074163, W92753
831248	Preferrably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 877 of SEQ ID NO:128, b is an integer of 15 to 891, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:128, and where b is greater than or equal to a + 14.	
831313	Preferrably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2447 of SEQ ID NO:129, b is an integer of 15 to 2461, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:129, and where b is greater than or equal to a + 14.	T61093, T97774, R13148, R31511, R32943, R33906, R33921, R37053, R44148, R44148, R74449, R79209, R79476, H12271, H27631, H30122, R84834, H63166, H71003, H71015, H83387, N23726, N23730, N23773, N52416, N66497, N67917, N68137, N73801, N99428, W95944, AA018712, AA020879, AA429721, AA470397, AA493243, AA507952, AA515358, AA583463, AA617991, AA618186, AA631437, AA566089, AA746085, AA837997, AA878863, AA922678, AA985597, AA947992, AI074096, C03207, C17030, C18106
831369	Preferrably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2183 of SEQ ID NO:130, b is an integer of 15 to 2197, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:130, and where b is greater than or equal to a + 14.	
831371	Preferrably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 450 of SEQ ID NO:131, b is an integer of 15 to 464, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:131, and where b is greater than or equal to a + 14.	
831373	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1936 of SEQ ID NO:132, b is an integer of 15 to 1950, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:132, and where b is greater than or equal to a + 14.	T50786, T50949, T53797, T53916, T64650, T71681, T71836, T71876, T71877, T74596, T74656, H30426, H46449, H46671, H46670, H46990, H50500, AA419051, AA423809, AA928986
831387	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2079 of SEQ ID NO:133, b is an integer of 15 to 2093, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:133, and where b is greater than or equal to a + 14.	
831410	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 715 of SEQ ID NO:134, b is an integer of 15 to 729, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:134, and where b is greater than or equal to a + 14.	
831448	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1175 of SEQ ID NO:135, b is an integer of 15 to 1189, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:135, and where b is greater than or equal to a + 14.	
831450	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1452 of SEQ ID NO:136, b is an integer of 15 to 1466, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:136, and where b is greater than or equal to a + 14.	
831472	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 126 of SEQ ID NO:137, b is an integer of 15 to 140, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:137, and where b is greater than or equal to a + 14.	
831473	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 4128 of SEQ ID NO:138, b is an integer of 15 to 4142, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:138, and where b is greater than or equal to a + 14.	
831474	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1733 of SEQ ID NO:139, b is an integer of 15 to 1747, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:139, and where b is greater than or equal to a + 14.	T66054, T89542, R10967, T78297, T83524, T97793, R13138, H08701, H10662, R82956, R96295, R98912, H66237, H79525, N31425, N36736, W76142, W81053, AA010227, AA011652, AA057613, AA057653, AA069088, AA083946, AA084193, AA126186, H70618, H79526, W72916, W80802, AA011433, AA057699, AA057752, AA069023
831494	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1226 of SEQ ID NO:140, b is an integer of 15 to 1240, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:140, and where b is greater than or equal to a + 14.	H14081, H14102, N34979, N42213, N43740, N68241, W69584, W69583, AA507828, AA877181, AA975100, AI000204
831506	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 657 of SEQ ID NO:141, b is an integer of 15 to 671, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:141, and where b is greater than or equal to a + 14.	AA035596, AA577792, AA903617, AA972775, AA996054, C00084
831533	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3251 of SEQ ID NO:142, b is an integer of 15 to 3265, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:142, and where b is greater than or equal to a + 14.	
831539	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 751 of SEQ ID NO:143, b is an integer of 15 to 765, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:143, and where b is greater than or equal to a + 14.	
831556	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1680 of SEQ ID NO:144, b is an integer of 15 to 1694, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:144, and where b is greater than or equal to a + 14.	H01879, H01880, H43546, H43547, H43548, N58813, N75148, AA428902, AA429101, AA278337, AA662009, AA928907, AA988624
831594	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 809 of SEQ ID NO:145. b is an integer of 15 to 823, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:145. and where b is greater than or equal to a + 14.	
831598	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1120 of SEQ ID NO:146. b is an integer of 15 to 1134, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:146. and where b is greater than or equal to a + 14.	
831608	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1472 of SEQ ID NO:147. b is an integer of 15 to 1486, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:147. and where b is greater than or equal to a + 14.	
831613	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 139 of SEQ ID NO:148. b is an integer of 15 to 153, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:148, and where b is greater than or equal to a + 14.	
831622	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 868 of SEQ ID NO:149, b is an integer of 15 to 882, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:149, and where b is greater than or equal to a + 14.	T40013, T40117, T55842, T55892, T58738, T58764, T58805, T58835, T58963, T60293, T60386, T61270, T61322, T61371, T61395, T61404, T61721, T61734, T61735, T61841, T61856, T61857, T61884, T62049, T62065, T62070, T62087, T62113, T62126, T62146, T41021, T62664, T62668, T62669, T62676, T62816, T62819, T62820, T62827, T64118, T64230, T64368, T64422, T64678, T64698, T64747, T67429, T67590, T67709, T67724, T67754, T67785, T67831, T67863, T67888, T67996, T68022, T68038, T68104, T68142, T68217, T68418, T68465, T68484, T68531, T68548, T68557, T68575, T68623, T68633, T68648, T68653, T68760, T68826, T68895, T68969, T68981, T69056, T69126, T69184, T69428, T69605, T69622, T69678, T69699, T70483, T70907, T70960, T71019, T71080, T71224, T71297, T71437, T71660, T71885, T71903, T71985, T72050, T72115, T72129, T72147, T72158, T72263, T72310, T72415, T72769, T72775, T72802, T72897, T72903, T72922, T72924, T73035, T73068, T73167, T73224, T73305, T73392, T73458, T73473, T73482, T73525, T73540, T73541, T73551, T73560, T73599, T73606, T73619, T73637, T73644, T73655, T73659, T73660, T73800,

		T73887, T73913, T73945, T73950, T74048, T74200, T74201, T74423, T74477, T74559, T74706, T74827, T99112, R05781, R05867, H47944, R95831, H60131, H65347, H65551, H68454, H68777, H73380, H73381, H79275, H79386, H82213, H82307, H93202, H93992, H93991, H94491, H94804, H95257, H95307, H95341, N28274, N58244, N68733, N77623, N80767, N91623, W07555, W80697, AA004677, AA004255, AA033869, AA034057, AA234464, AA491842, C20927
831631	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1494 of SEQ ID NO:150, b is an integer of 15 to 1508, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:150, and where b is greater than or equal to a + 14.	
831632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1218 of SEQ ID NO:151, b is an integer of 15 to 1232, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:151, and where b is greater than or equal to a + 14.	T60158, T60218, T62213, T62652, T62877, T62966, T63329, T63951, T64542, T64634, T65965, T90119, T91565, T91610, T92138, T94160, T94999, T90219, T83025, T84028, T84029, T84511, R22325, R22619, R22620, R25250, R25595, R26992, R27328, R32850, R32954, R33282, R44282, R47779, R48151, R48152, R48322, R48428, R48538, R50415, R52277, R52278, R54608, R44282, R55376, R70352, R72103, R72155, R72280, R72317, R72367, R72368, R72371, R72372, R72716, R73784, R74375, R77393, R77394, R77892, R77987, R81485, R81725, H05676, H15941, H22149, H22193, H24533, H25059, H26810, H27743, H27803, H28012, H28066, H28290, H28291, H30654, H39748, H39761, H41932, H41979, H42063, H42642, H42766, H42767, H44628, H45776, H45777, H46386, H46404, R93135, R93942, R94660, R94661, H50708, H50709, H50720, H50812, H50811, H50826, H61352, H62379, H63665, H63944, H66336, H66385, H70746, H73887, H74080, H74176, H82646, H82647, H86555, H87065, H87719, H91147, H91197, H93078, H93211, H98788, N24993, N25111, N30229, N32159, N34033, N36553, N41829, N42292, N46951, N49340, N52921, N55462, N57121, N69863, N76837, N80667, N92844, N93333, N93683, N94449, N95075, W16427, W15325, W23470, W23480, W25070, W25186, W30795,

		W38675, W39219, W39393, W69270, W69557, AA019864, AA022662, AA022669, AA022768, AA025335, AA024417, AA031282, AA031281, AA032192, AA039752, AA040328, AA040307, AA041359, AA041442, AA057720, AA074855, AA086192, AA099717, AA099716, AA100416, AA142927, AA143150, AA149895, AA150239, AA150313, AA176193, AA459294, AA464165, AA425845, AA425899, AA428397, AA430393, AA427364, AA469113, AA505259, AA515918, AA516032, AA527677, AA533908, AA541266, AA554671, AA555247, AA557794, AA565267, AA582247, AA584415, AA588477, AA593255, AA595311, AA595376, AA604354, AA622137, AA573444, AA574244, AA732469, AA740323, AA741360, AA742872, AA749432, AA807903, AA808285, AA872498, AA873181, AA878139, AA878294, AA909748, AA937058, AA987672, AA994225, AI076066, W07696
831653	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 985 of SEQ ID NO:152, b is an integer of 15 to 999, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:152, and where b is greater than or equal to a + 14.	
831655	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1198 of SEQ ID NO:153, b is an integer of 15 to 1212, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:153, and where b is greater than or equal to a + 14.	N95539, W24228, W37689, AA019086, AA430215
831708	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2347 of SEQ ID NO:154, b is an integer of 15 to 2361, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:154, and where b is greater than or equal to a + 14.	
831738	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1817 of SEQ ID NO:155, b is an integer of 15 to 1831, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:155, and where b is greater than or equal to a + 14.	

831741	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1172 of SEQ ID NO:156, b is an integer of 15 to 1186, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:156, and where b is greater than or equal to a + 14.	T47689, T80213, H11356, H13411, R86865, R87546, N35663, AA081442, AA161001, C17978, C18946
831754	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1434 of SEQ ID NO:157, b is an integer of 15 to 1448, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:157, and where b is greater than or equal to a + 14.	
831760	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 990 of SEQ ID NO:158, b is an integer of 15 to 1004, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:158, and where b is greater than or equal to a + 14.	R73907, R74000, N64405, AA196765, AA232516, AA806432, AA837776, AI017699
831780	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1495 of SEQ ID NO:159, b is an integer of 15 to 1509, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:159, and where b is greater than or equal to a + 14.	AA100654, AA112750, AA594472, AA731487
831796	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2146 of SEQ ID NO:160, b is an integer of 15 to 2160, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:160, and where b is greater than or equal to a + 14.	H14891, W74005, AA623010, D80585, AI096496, W38434
831800	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3595 of SEQ ID NO:161, b is an integer of 15 to 3609, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:161, and where b is greater than or equal to a + 14.	
831807	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1589 of SEQ ID NO:162, b is an integer of 15 to 1603, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:162, and where b is greater than or equal to a + 14.	
831812	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 839 of SEQ ID NO:163, b is an integer of 15 to 853, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:163, and where b is greater than or equal to a + 14.	
831813	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1903 of SEQ ID NO:164, b is an integer of 15 to 1917, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:164, and where b is greater than or equal to a + 14.	H14269. AA069213. AA808661
831830	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2406 of SEQ ID NO:165, b is an integer of 15 to 2420, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:165, and where b is greater than or equal to a + 14.	H04695. AA112742. AA251641, AA506539
831860	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2047 of SEQ ID NO:166, b is an integer of 15 to 2061, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:166, and where b is greater than or equal to a + 14.	
831872	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2553 of SEQ ID NO:167, b is an integer of 15 to 2567, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:167, and where b is greater than or equal to a + 14.	R15368, R36227, R36228, R36669, R39751, H12331, H12382, H47986, R84945, R97224, R97223, W78107, AA149874. AA193466. AA193348. AA287444. AA535607. AA687414. AA689396. AA748665, AA809715
831896	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2310 of SEQ ID NO:168, b is an integer of 15 to 2324, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:168, and where b is greater than or equal to a + 14.	R59635, N28389, AA158646, AA158659, AA188594, AA190705, AA459426, AA465652
831928	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1770 of SEQ ID NO:169, b is an integer of 15 to 1784, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:169, and where b is greater than or equal to a + 14.	
831949	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1282 of SEQ ID NO:170, b is an integer of 15 to 1296, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:170, and where b is greater than or equal to a + 14.	
831950	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1883 of SEQ ID NO:171, b is an integer of 15 to 1897, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:171, and where b is greater than or equal to a + 14.	
831953	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1709 of SEQ ID NO:172, b is an integer of 15 to 1723, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:172, and where b is greater than or equal to a + 14.	
831975	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1402 of SEQ ID NO:173, b is an integer of 15 to 1416, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:173, and where b is greater than or equal to a + 14.	
832036	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1942 of SEQ ID NO:174, b is an integer of 15 to 1956, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:174, and where b is greater than or equal to a + 14.	R60820, R78776, R79082, H01912, H04427, N34789, N44513, W20183, W35150, AA159701, AA159628, AA470753, AA659808
832047	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1675 of SEQ ID NO:175, b is an integer of 15 to 1689, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:175, and where b is greater than or equal to a + 14.	R21952, R21968, R26963, R78028, H75703, H75632, H84015, H88136, H88135, H94007, H95012, N24834, N30818, N31761, N41592, N79533, W16686, W24639, W38979, W87777, W87875, AA121146, AA122426, AA131874, AA131978, AA147083, AA147140, AA282507, AA282605, AA558945, H84016, AA587558, AA830662, AA866026, AA917653, AI017813, C06340
832078	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1002 of SEQ ID NO:176, b is an integer of 15 to 1016, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:176, and where b is greater than or equal to a + 14.	

832100	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1350 of SEQ ID NO:177, b is an integer of 15 to 1364, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:177, and where b is greater than or equal to a + 14.	
832104	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 726 of SEQ ID NO:178, b is an integer of 15 to 740, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:178, and where b is greater than or equal to a + 14.	
832268	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1396 of SEQ ID NO:179, b is an integer of 15 to 1410, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:179, and where b is greater than or equal to a + 14.	
832270	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1479 of SEQ ID NO:180, b is an integer of 15 to 1493, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:180, and where b is greater than or equal to a + 14.	
832279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2026 of SEQ ID NO:181, b is an integer of 15 to 2040, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:181, and where b is greater than or equal to a + 14.	
832317	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 955 of SEQ ID NO:182, b is an integer of 15 to 969, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:182, and where b is greater than or equal to a + 14.	R81508, H12476, H86945, AA053747, AA115783, AA133749, AA134163, AA134164, AA224985, AA228334, AA228423, AA229297, AA640471, AA657793, AA687568, AA904162, AA983632
832354	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1438 of SEQ ID NO:183, b is an integer of 15 to 1452, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:183, and where b is greater than or equal to a + 14.	
832364	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2105 of SEQ ID NO:184, b is an integer of 15 to 2119, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:184, and where b is greater than or equal to a + 14.	
832378	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1311 of SEQ ID NO:185, b is an integer of 15 to 1325, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:185, and where b is greater than or equal to a + 14.	
832385	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 419 of SEQ ID NO:186, b is an integer of 15 to 433, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:186, and where b is greater than or equal to a + 14.	
832428	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 845 of SEQ ID NO:187, b is an integer of 15 to 859, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:187, and where b is greater than or equal to a + 14.	AA031420
832485	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 819 of SEQ ID NO:188, b is an integer of 15 to 833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:188, and where b is greater than or equal to a + 14.	R63025, R66741, H53264, H53265, H53769, H53822, H54405, H54489, H81182, H91282, AA526672, H81181
832494	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2197 of SEQ ID NO:189, b is an integer of 15 to 2211, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:189, and where b is greater than or equal to a + 14.	T61040, T61591, T90055, T90157, T92840, T93714, T96177, T77726, H04686, H05450, H06997, H20176, H20366, R92666, H65144, H92413, N64053, N64060, N66714, N71338, N71388, N79742, N95497, N99884, W07259, W24989, W37394, W37657, W40208, W40260, W40532, W45430, W56165, W60427, W60986, W61080, W63739, W72328, W73757, W74394, AA025512, AA026057, AA065019, AA069295, AA069798, AA069845, AA070441, AA075793, AA083393, AA083394, AA084576, AA086181, AA099019, AA099097, AA099493, AA102003, AA100395, AA100554, AA100555, AA100638, AA101578, AA113226, AA113811, AA115645, AA115646.

		AA115888. AA115889. AA122231. AA121108. AA121596. AA121671. AA121743. AA126075. AA126102. AA126181. AA126295. AA126404. AA129470. AA129665. AA133945. AA133946. AA146752. AA155947. AA157140. AA157228. AA159947. AA160900. AA164889. AA164890. AA164840. AA164839. AA172107. AA182040. AA171714. AA187244. AA187376. AA186418. AA188846. AA189131. AA196155. AA196257. AA196611. AA196789. AA196961. AA223155. AA223415. AA226816. AA226856. AA227026. AA227109. AA227208. AA243161. AA243205. AA428759. AA429347. AA514858. AA535250. AA555125. AA565075. AA565168. AA581531. AA587192. AA576761. AA580523. AA659699. AA688240. AA689484. AA689543. AA689313. AA729979. AA740203. AA747258. AA747399. AA747993. AA837961. AA865930. AA906561. AA910350. AA919085. AA931143. AA999884. A1051141. F19298. W22294, W22759. W22970. W25820. W73709, C02713. C02766. C03390. C03613, C04202. C05262. C05272. R28954. R29028. R29032. AA062628. AA090039. C18989
832512	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1645 of SEQ ID NO:190. b is an integer of 15 to 1659, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:190, and where b is greater than or equal to a + 14.	
832515	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3880 of SEQ ID NO:191, b is an integer of 15 to 3894, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:191, and where b is greater than or equal to a + 14.	
832526	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 681 of SEQ ID NO:192, b is an integer of 15 to 695, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:192, and where b is greater than or equal to a + 14.	
832575	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	R28543. R28684. R55782. R55862, R62797. R62843. R67670. R71154.

	sequence described by the general formula of a-b, where a is any integer between 1 to 3117 of SEQ ID NO:193, b is an integer of 15 to 3131, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:193, and where b is greater than or equal to a + 14.	R71651, N20642, N24838, N35562, N29014, N31768, N34161, N57560, N72111, W00338, W00374, W30889, W52729, W59982, W68047, W68189, AA019459, AA043870, AA044336, AA045040, AA045041, AA115599, AA115134, AA131177, AA165259, AA165260, AA165191, AA165192, AA164549, AA164550, AA261988, AA424972, AA279863, AA458832, AA459024, AA505193, AA507542, AA514388, AA622542, AA689232, AA689233, AA804910, AA807169, AA832321, AA878091, AA904023, AA936069, AA936071, AA946621, C00143, N86645, AA010988, AA641236, AA641464, C18301
832576	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2044 of SEQ ID NO:194, b is an integer of 15 to 2058, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:194, and where b is greater than or equal to a + 14.	
832588	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 817 of SEQ ID NO:195, b is an integer of 15 to 831, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:195, and where b is greater than or equal to a + 14.	
832634	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 947 of SEQ ID NO:196, b is an integer of 15 to 961, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:196, and where b is greater than or equal to a + 14.	
832728	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 592 of SEQ ID NO:197, b is an integer of 15 to 606, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:197, and where b is greater than or equal to a + 14.	
833094	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 379 of SEQ ID NO:198, b is an integer of 15 to 393, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:198, and where b is greater than or equal to a + 14.	

833395	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1047 of SEQ ID NO:199, b is an integer of 15 to 1061, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:199, and where b is greater than or equal to a + 14.	
834326	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1345 of SEQ ID NO:200, b is an integer of 15 to 1359, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:200, and where b is greater than or equal to a + 14.	
834583	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 712 of SEQ ID NO:201, b is an integer of 15 to 726, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:201, and where b is greater than or equal to a + 14.	
834944	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2700 of SEQ ID NO:202, b is an integer of 15 to 2714, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:202, and where b is greater than or equal to a + 14.	
835012	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 408 of SEQ ID NO:203, b is an integer of 15 to 422, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:203, and where b is greater than or equal to a + 14.	
835104	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2325 of SEQ ID NO:204, b is an integer of 15 to 2339, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:204, and where b is greater than or equal to a + 14.	
835332	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1641 of SEQ ID NO:205, b is an integer of 15 to 1655, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:205, and where b is greater than or equal to a + 14.	
835487	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 5131 of SEQ ID NO:206, b is an integer of 15 to 5145, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:206, and where b is greater than or equal to a + 14.	
836182	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 473 of SEQ ID NO:207, b is an integer of 15 to 487, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:207, and where b is greater than or equal to a + 14.	
836522	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2282 of SEQ ID NO:208, b is an integer of 15 to 2296, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:208, and where b is greater than or equal to a + 14.	
836655	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 611 of SEQ ID NO:209, b is an integer of 15 to 625, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:209, and where b is greater than or equal to a + 14.	
836787	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1537 of SEQ ID NO:210, b is an integer of 15 to 1551, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:210, and where b is greater than or equal to a + 14.	W56241, W56321, AA009901, AA521313, AA732599, AA730271, AA766911, AA767313, W27009
836789	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 997 of SEQ ID NO:211, b is an integer of 15 to 1011, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:211, and where b is greater than or equal to a + 14.	T68817, R22374, R27362, H38950, R89148, R91088, H68416, H93594, N33889, N47045, N56761, W19886, W44630, W61370, W86385, AA036993, AA065062, AA101017, AA121107, AA130485, AA147474, AA160596, AA282977
838577	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1625 of SEQ ID NO:212, b is an integer of 15 to 1639, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:212, and where b is greater than or equal to a + 14.	T53501, T40735, T63398, T63985, T64053, T64155, T64284, T93511, T94941, T94995, T96340, R00890, R01553, R12738, R12739, R39790, R54423, R66373, R66595, R67104, R67219, R79151, R79152, R82180, R82224, R82470, R82471, H01963, H02048, H02758, H02759, H05982, H19484, H19567, H19882, H19900, H44901, H44938, H44978, H46289, H46871, H49538.

	H49781, H53114, H53220, H54300, H56079, H56279, H79695, H79696, N23140, N25755, N25850, N26983, N29784, N32719, N36477, N40104, N42924, N44580, N50724, N55052, N67751, N93444, N98425, N98537, W02803, W21105, W23673, W30688, W30899, W35106, W45448, W45449, W45661, W44441, W46823, W46872, W47373, W47374, W52205, W58331, W58652, W96332, AA007386, AA007676, AA011363, AA016311, AA017511, AA018464, AA019899, AA025040, AA025039, AA029796, AA029797, AA031472, AA035395, AA035396, AA037272, AA040791, AA041228, AA042893, AA043029, AA055565, AA056185, AA056186, AA056621, AA056726, AA069193, AA079705, AA082517, AA084044, AA084043, AA115273, AA115056, AA132031, AA132153, AA149267, AA149284, AA149378, AA158093, AA158103, AA158364, AA158904, AA158905, AA165106, AA220957, AA235312, AA251169, AA421302, AA421425, AA428706, AA429291, AA513790, AA531603, AA551736, AA554236, AA605236, AA604674, AA604939, AA612935, AA617731, AA627300, AA687527, AA732095, AA740760, AA765135, AA765136, AA765296, AA765891, AA888144, AA908665, AA928038, AA936934, AA961143, AA987647, AA975856, W03595, C03206, C18055, AA164690, AA218956, AA291352, AA292329, AA293276, AA393988, AA398076, AA410772, D12417, AA442678, AA442969, AA454814, AA454888, AA482370, AA486098, AA486161, AA625879, AA678365, AA679281, AA703505, AA722872, AA732793, AA989559, AI003448, AI014938, AI022070, AI084792, AI092360
838717	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2113 of SEQ ID NO:213, b is an integer of 15 to 2127, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:213, and where b is greater than or equal to a + 14.
839008	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1152 of SEQ ID

	NO:214. b is an integer of 15 to 1166, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:214, and where b is greater than or equal to a + 14.	
840063	Prefrably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3309 of SEQ ID NO:215, b is an integer of 15 to 3323, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:215, and where b is greater than or equal to a + 14.	
840533	Prefrably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1394 of SEQ ID NO:216, b is an integer of 15 to 1408, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:216, and where b is greater than or equal to a + 14.	
840669	Prefrably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2097 of SEQ ID NO:217, b is an integer of 15 to 2111, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:217, and where b is greater than or equal to a + 14.	T71029, T79145, T79226, T99989, R59589, R61735, R61734, R66190, R67070, H16201, H16200, H22960, H84137, H85574, H98850, N23572, N26340, N56614, W72249, W76334, W86530, W87654, W87653, AA057869, AA122103, AA129545, AA136524, AA137122, AA429808, AA525242, AA558970, H99223, AA584317, AA595168, AA825180, AA931521, AA938437, AI017369, N29659, N68604, W86674, AA007246
841140	Prefrably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2479 of SEQ ID NO:218, b is an integer of 15 to 2493, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:218, and where b is greater than or equal to a + 14.	
841386	Prefrably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1245 of SEQ ID NO:219, b is an integer of 15 to 1259, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:219, and where b is greater than or equal to a + 14.	AA429393, AA429394, AA493187, AA807096, AA836046
841480	Prefrably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1835 of SEQ ID NO:220, b is an integer of 15 to 1849, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:220, and where b is greater than or equal to a + 14.	
841509	Prefrably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1253 of SEQ ID NO:221, b is an integer of 15 to 1267, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:221, and where b is greater than or equal to a + 14.	
841616	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 740 of SEQ ID NO:222, b is an integer of 15 to 754, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:222, and where b is greater than or equal to a + 14.	
841900	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1244 of SEQ ID NO:223, b is an integer of 15 to 1258, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:223, and where b is greater than or equal to a + 14.	R87848, AA806230, Z28656
842054	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 570 of SEQ ID NO:224, b is an integer of 15 to 584, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:224, and where b is greater than or equal to a + 14.	
843061	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3435 of SEQ ID NO:225, b is an integer of 15 to 3449, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:225, and where b is greater than or equal to a + 14.	
843544	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1852 of SEQ ID NO:226, b is an integer of 15 to 1866, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:226, and where b is greater than or equal to a + 14.	
844092	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1050 of SEQ ID NO:227, b is an integer of 15 to 1064, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:227, and where b is greater than or equal to a + 14.	
844270	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 359 of SEQ ID NO:228, b is an integer of 15 to 373, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:228, and where b is greater than or equal to a + 14.	
844604	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2830 of SEQ ID NO:229, b is an integer of 15 to 2844, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:229, and where b is greater than or equal to a + 14.	
844685	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1784 of SEQ ID NO:230, b is an integer of 15 to 1798, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:230, and where b is greater than or equal to a + 14.	
844855	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1809 of SEQ ID NO:231, b is an integer of 15 to 1823, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:231, and where b is greater than or equal to a + 14.	
845101	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 956 of SEQ ID NO:232, b is an integer of 15 to 970, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:232, and where b is greater than or equal to a + 14.	
845141	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 953 of SEQ ID NO:233, b is an integer of 15 to 967, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:233, and where b is greater than or equal to a + 14.	
845220	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2149 of SEQ ID NO:234, b is an integer of 15 to 2163, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:234, and where b is greater than or equal to a + 14.	R70310, H02204, H28992, H29096, W67797, W67855, W72320, AA459289, AA459519, AA430385, AA746169
845434	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 1307 of SEQ ID NO:235. b is an integer of 15 to 1321, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:235, and where b is greater than or equal to a + 14.	
845510	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 669 of SEQ ID NO:236, b is an integer of 15 to 683, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:236, and where b is greater than or equal to a + 14.	
845600	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2101 of SEQ ID NO:237, b is an integer of 15 to 2115, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:237, and where b is greater than or equal to a + 14.	
845882	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1628 of SEQ ID NO:238, b is an integer of 15 to 1642, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:238, and where b is greater than or equal to a + 14.	
846007	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 454 of SEQ ID NO:239, b is an integer of 15 to 468, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:239, and where b is greater than or equal to a + 14.	H81424
846280	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1315 of SEQ ID NO:240, b is an integer of 15 to 1329, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:240, and where b is greater than or equal to a + 14.	
846286	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1638 of SEQ ID NO:241, b is an integer of 15 to 1652, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:241, and where b is greater than or equal to a + 14.	
846388	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1932 of SEQ ID	

NO:242. b is an integer of 15 to 1946, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:242, and where b is greater than or equal to a + 14.

Polynucleotide and Polypeptide Variants

The present invention is directed to variants of the polynucleotide sequence disclosed in SEQ ID NO:X or the complementary strand thereto, and/or the cDNA sequence contained in a cDNA clone contained in the deposit.

5 The present invention also encompasses variants of a colon and/or colon cancer polypeptide sequence disclosed in SEQ ID NO:Y, a polypeptide sequence encoded by the polynucleotide sequence in SEQ ID NO:X, and/or a polypeptide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide 10 or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

The present invention is also directed to nucleic acid molecules which comprise, or alternatively consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 95%, 96%, 15 97%, 98%, 99% or 100%, identical to, for example, the nucleotide coding sequence in SEQ ID NO:X or the complementary strand thereto, the nucleotide coding sequence of the related cDNA contained in a deposited library or the complementary strand thereto, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a nucleotide 20 sequence encoding the polypeptide encoded by the cDNA in the related cDNA contained in a deposited library, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polypeptides encoded by these nucleic acid molecules are also encompassed by the invention. In another embodiment, the invention encompasses nucleic acid molecules which comprise or alternatively consist of, a 25 polynucleotide which hybridizes under stringent hybridization conditions, or alternatively, under low stringency conditions, to the nucleotide coding sequence in SEQ ID NO:X, the nucleotide coding sequence of the related cDNA clone contained in a deposited library, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a 30 nucleotide sequence encoding the polypeptide encoded by the cDNA in the related cDNA clone contained in a deposited library, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polynucleotides which

hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

The present invention is also directed to polypeptides which comprise, or alternatively 5 consist of, an amino acid sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to, for example, the polypeptide sequence shown in SEQ ID NO:Y, a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the cDNA in the related cDNA clone contained in a deposited library, and/or polypeptide fragments of any of these polypeptides (e.g., those fragments described 10 herein). Polynucleotides which hybridize to the complement of the nucleic acid molecules encoding these polypeptides under stringent hybridization conditions, or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

By a nucleic acid having a nucleotide sequence at least, for example, 95% "identical" 15 to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the nucleic acid is identical to the reference sequence except that the nucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a nucleic acid having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 20 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be, for example, an entire sequence referred to in Table 1, an ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is 25 at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global 30 sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be

compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identiy are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30. Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size 5 Penalty 0.05, Window Size=500 or the lenght of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the 10 subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. 15 This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of 20 manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 25 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which 30 are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other

manual corrections are to be made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that 5 the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95%-identical-to-a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur 10 at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence in SEQ ID 15 NO:Y or a fragment thereof, the amino acid sequence encoded by the nucleotide sequence in SEQ ID NO:X or a fragment thereof, or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library, or a fragment thereof, can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present 20 invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci.6:237- 245(1990)). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a 25 FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal 30 deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences

truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is 5 matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the 10 query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the 15 subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent 20 identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject 25 sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce 30 silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which less than 50, less

than 40, less than 30, less than 20, less than 10, or 5-50, 5-25, 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).
5

- Naturally occurring variants are called "allelic variants." and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present invention.
10 Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, as discussed herein, one or more amino acids can be deleted
15 from the N-terminus or C-terminus of the polypeptide of the present invention without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the
20 carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1 α . They used random mutagenesis to generate over 3,500 individual IL-1 α mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in
25 activity from wild-type.
30

Furthermore, as discussed herein, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more

biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or 5 C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show a functional activity (e.g., biological activity) of the polypeptide of the invention of which they are a variant. Such variants include deletions, insertions, inversions, repeats, and substitutions 10 selected according to general rules known in the art so as have little effect on activity.

The present application is directed to nucleic acid molecules at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein or fragments thereof, (e.g., including but not limited to fragments encoding a polypeptide having the amino acid sequence of an N and/or C terminal deletion), irrespective of whether 15 they encode a polypeptide having functional activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having functional activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe or a polymerase chain reaction (PCR) primer. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having functional activity 20 include, inter alia, (1) isolating a gene or allelic or splice variants thereof in a cDNA library; (2) in situ hybridization (e.g., "FISH") to metaphase chromosomal spreads to provide precise chromosomal location of the gene, as described in Verma et al., Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York (1988); and (3) Northern Blot analysis for detecting mRNA expression in specific tissues.

Preferred, however, are nucleic acid molecules having sequences at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein, which do, in fact, encode a polypeptide having a functional activity of a polypeptide 25 of the invention.

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art 30 will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to, for example, the nucleic acid sequence of the cDNA in the related cDNA clone contained in a

deposited library, the nucleic acid sequence referred to in Table 1 (SEQ ID NO:X), or fragments thereof, will encode polypeptides "having functional activity." In fact, since degenerate variants of any of these nucleotide sequences all encode the same polypeptide, in many instances, this will be clear to the skilled artisan even without performing the above 5 described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having functional activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as 10 further described below.

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid 15 sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have 20 been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For 25 example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly 30 tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side

chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln. replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.. Besides conservative amino-acid-substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as, for example, an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a polypeptide having an amino acid sequence which contains at least one amino acid substitution, but not more than 50 amino acid substitutions, even more preferably, not more than 40 amino acid substitutions, still more preferably, not more than 30 amino acid substitutions, and still even more preferably, not more than 20 amino acid substitutions. Of course it is highly preferable for a polypeptide to have an amino acid sequence which comprises the amino acid sequence of a polypeptide of SEQ ID NO:Y, an amino acid sequence encoded by SEQ ID NO:X, and/or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library which contains, in order of ever-increasing preference, at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1

amino acid substitutions. In specific embodiments, the number of additions, substitutions, and/or deletions in the amino acid sequence of SEQ ID NO:Y or fragments thereof (e.g., the mature form and/or other fragments described herein), an amino acid sequence encoded by SEQ ID NO:X or fragments thereof, and/or the amino acid sequence encoded by the cDNA in 5 the related cDNA clone contained in a deposited library or fragments thereof, is 1-5, 5-10, 5-25, 5-50, 10-50 or 50-150, conservative amino acid substitutions are preferable.

Polynucleotide and Polypeptide Fragments

The present invention is also directed to polynucleotide fragments of the colon and/or 10 colon cancer polynucleotides (nucleic acids) of the invention. In the present invention, a "polynucleotide fragment" refers, for example, to a polynucleotide having a nucleic acid sequence which: is a portion of the cDNA contained in a deposited cDNA clone; or is a portion of a polynucleotide sequence encoding the polypeptide encoded by the cDNA contained in a deposited cDNA clone; or is a portion of the polynucleotide sequence in SEQ 15 ID NO:X or the complementary strand thereto; or is a polynucleotide sequence encoding a portion of the polypeptide of SEQ ID NO:Y; or is a polynucleotide sequence encoding a portion of a polypeptide encoded by SEQ ID NO:X or the complementary strand thereto. The nucleotide fragments of the invention are preferably at least about 15 nt, and more 20 preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt, at least about 50 nt, at least about 75 nt, at least about 100 nt, at least about 125 nt or at least about 150 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from, for example, the sequence contained in the cDNA in a related cDNA clone contained in a deposited library, the nucleotide sequence shown in SEQ ID NO:X or the complementary stand thereto. In this 25 context "about" includes the particularly recited value or a value larger or smaller by several (5, 4, 3, 2, or 1) nucleotides. These nucleotide fragments have uses that include, but are not limited to, as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., at least 150, 175, 200, 250, 500, 600, 1000, or 2000 nucleotides in length) are also encompassed by the invention.

30 Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-

- 400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900,
901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300,
1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-
1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050,
5 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-
2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800,
2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-
3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550,
3551-3600, 3601-3650, 3651-3700, 3701-3750, 3751-3800, 3801-3850, 3851-3900, 3901-
10 3950, 3951-4000, 4001-4050, 4051-4100, and 4101 to the end of SEQ ID NO:X, or the
complementary strand thereto. In this context "about" includes the particularly recited range
or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at
both termini. Preferably, these fragments encode a polypeptide which has a functional
activity (e.g., biological activity) of the polypeptide encoded by the polynucleotide of which
15 the sequence is a portion. More preferably, these fragments can be used as probes or primers
as discussed herein. Polynucleotides which hybridize to one or more of these nucleic acid
molecules under stringent hybridization conditions or alternatively, under lower stringency
conditions, are also encompassed by the invention, as are polypeptides encoded by these
polynucleotides or fragments.
- 20 Moreover, representative examples of polynucleotide fragments of the invention,
include, for example, fragments comprising, or alternatively consisting of, a sequence from
about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-
400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900,
901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300,
25 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-
1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050,
2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-
2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800,
2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-
3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550,
3551-3600, 3601-3650, 3651-3700, 3701-3750, 3751-3800, 3801-3850, 3851-3900, 3901-
30 3950, 3951-4000, 4001-4050, 4051-4100, and 4101 to the end of the cDNA nucleotide

sequence contained in the deposited cDNA clone, or the complementary strand thereto. In this context "about" includes the particularly recited range, or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity) of

5 the polypeptide encoded by the cDNA nucleotide sequence contained in the deposited cDNA clone. More preferably, these fragments can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these fragments under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides or

10 fragments.

In the present invention, a "polypeptide fragment" refers to an amino acid sequence which is a portion of that contained in SEQ ID NO:Y, a portion of an amino acid sequence encoded by the polynucleotide sequence of SEQ ID NO:X, and/or encoded by the cDNA contained in the related cDNA clone contained in a deposited library. Protein (polypeptide) fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, an amino acid sequence from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-640, 641-660, 661-680, 681-700, 701-720, 721-740, 741-760, 761-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981-1000, 1001-1020, 1021-1040, 1041-1060, 1061-1080, 1081-1100, 1101-1120, 1121-1140, 1141-1160, 1161-1180, 1181-1200, 1201-1220, 1221-1240, 1241-1260, 1261-1280, 1281-1300, 1301-1320, 1321-1340, 1341-1360, and 1361 to the end of SEQ ID NO:Y. Moreover, polypeptide fragments of the invention may be at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges or values, or ranges or values larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either terminus or at both termini. Polynucleotides encoding these polypeptide fragments are also encompassed by the invention.

Even if deletion of one or more amino acids from the N-terminus of a protein results in modification or loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, polypeptide fragments of the invention include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotides encoding these polypeptide fragments are also preferred.

The present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X, and/or a polypeptide encoded by the cDNA contained in the related cDNA clone contained in a deposited library). In particular, N-terminal deletions may be described by the general formula m-q, where q is a whole integer representing the total number of amino acid residues in a polypeptide of the invention (e.g., the polypeptide disclosed in SEQ ID NO:Y), and m is defined as any integer ranging from 2 to q-6. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification or loss of one or more biological functions of

the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example the ability of the shortened mutein to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the 5 complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides 10 composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues from the carboxy terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X, and/or a polypeptide encoded by the cDNA contained 15 in the related cDNA referenced in Table 1). In particular, C-terminal deletions may be described by the general formula 1-n, where n is any whole integer ranging from 6 to q-1, and where n corresponds to the position of an amino acid residue in a polypeptide of the invention. Polynucleotides encoding these polypeptides are also encompassed by the invention.

20 In addition, any of the above described N- or C-terminal deletions can be combined to produce a N- and C-terminal deleted polypeptide. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini, which may be described generally as having residues m-n of a polypeptide encoded by SEQ ID NO:X (e.g., including, but not limited to, the preferred polypeptide disclosed as SEQ ID 25 NO:Y), and/or the cDNA in the related cDNA clone contained in a deposited library, where n and m are integers as described above. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Any polypeptide sequence contained in the polypeptide of SEQ ID NO:Y, encoded by the polynucleotide sequences set forth as SEQ ID NO:X, or encoded by the cDNA in the 30 related cDNA clone contained in a deposited library may be analyzed to determine certain preferred regions of the polypeptide. For example, the amino acid sequence of a polypeptide encoded by a polynucleotide sequence of SEQ ID NO:X, or the cDNA in a deposited cDNA

clone may be analyzed using the default parameters of the DNASTAR computer algorithm (DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715 USA; <http://www.dnastar.com/>).

Polypeptide regions that may be routinely obtained using the DNASTAR computer algorithm include, but are not limited to, Garnier-Robson alpha-regions, beta-regions, 5 turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Eisenberg alpha- and beta-amphipathic-regions, Karplus-Schulz flexible regions, Emini surface-forming regions and Jameson-Wolf regions of high antigenic index. Among highly preferred polynucleotides of the invention in this regard are those that encode polypeptides comprising regions that 10 combine several structural features, such as several (e.g., 1, 2, 3 or 4) of the features set out above.

Additionally, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Emini surface-forming regions, and Jameson-Wolf regions of high antigenic index (i.e., containing four or more contiguous amino acids having an antigenic index of greater than or equal to 15 1.5, as identified using the default parameters of the Jameson-Wolf program) can routinely be used to determine polypeptide regions that exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from data by DNASTAR analysis by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the 20 process of initiation of an immune response.

Preferred polypeptide fragments of the invention are fragments comprising, or alternatively consisting of, an amino acid sequence that displays a functional activity of the polypeptide sequence of which the amino acid sequence is a fragment.

By a polypeptide demonstrating a "functional activity" is meant, a polypeptide 25 capable of displaying one or more known functional activities associated with a full-length (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the 30 invention, and ability to bind to a receptor or ligand for a polypeptide.

Other preferred polypeptide fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an

activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

In preferred embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the antigenic fragments of the polypeptide of SEQ ID NO:Y. or portions thereof. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Table 4.

Sequence/ Contig ID	Predicted Epitopes
500802	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 774 as residues: Gln-1 to Ser-17, Ser-19 to Ile-25, Leu-29 to Arg-41, Ser-46 to Glu-57.
553147	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 776 as residues: Phe-1 to Ile-20.
558860	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 777 as residues: Ser-6 to Arg-11.
561730	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 778 as residues: Asn-1 to Arg-7, Leu-28 to Pro-45.
585938	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 779 as residues: Arg-10 to Ser-23, Gln-69 to His-74.
587785	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 780 as residues: Ile-1 to Ser-11, Leu-20 to Thr-30, Cys-74 to Cys-82, Leu-94 to Glu-110.
588916	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 781 as residues: Val-43 to Pro-55, Glu-92 to Ser-99.
613825	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 782 as residues: Asn-1 to Trp-11, Ser-15 to Gln-22, Ser-43 to Ala-51, Lys-58 to Gly-66.
639090	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 783 as residues: Ser-29 to Ser-35, Pro-43 to Gly-48, Gln-60 to Ser-65.
659544	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 785 as residues: Leu-10 to Glu-15, His-19 to Glu-26.
659739	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 786 as residues: Lys-70 to His-78, Lys-149 to Asn-154, Gly-209 to Leu-217, Lys-248 to Val-255, Ile-259 to Arg-264, Arg-280 to Ala-287.
661057	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 787 as residues: Cys-59 to Arg-64, Gly-110 to Asp-115, Pro-127 to Trp-132.
661313	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 788 as residues: Glu-1 to Phe-7, Lys-42 to Leu-48.
666316	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 789 as residues: Lys-27 to Asn-52.
669229	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 790 as residues: Asp-1 to Phe-12, Val-92 to Ser-103.
670471	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 791 as residues: Lys-75 to Asp-81, Glu-145 to Gln-156, Glu-163 to Arg-170, Lys-225 to Leu-231.
676611	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 792 as residues: Tyr-4 to Lys-12, Thr-23 to Asn-31, Val-52 to Thr-63, Arg-90 to Met-95.
691240	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 793 as residues: Pro-74 to Glu-79, Ser-116 to Lys-121.
702977	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 794 as residues: Pro-8 to Tyr-20.
709517	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 795 as residues: Leu-7 to Gly-12, Cys-20 to His-27.
714730	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 796 as residues: Pro-14 to Arg-23, Ala-171 to Ser-178.
714834	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 797 as residues: Ala-6 to Gly-12, Gln-18 to Arg-32.
719584	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 799 as residues: Pro-22 to Ile-31.
724637	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 800 as residues: Val-11 to Arg-34, Asn-54 to Cys-59.
728392	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 801 as

	residues: Arg-31 to Glu-45. Gly-76 to Pro-88. Asn-143 to Asp-148.
738716	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 802 as residues: Pro-40 to Pro-46.
739056	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 803 as residues: Ser-28 to Ala-33. Pro-44 to Phe-49. Arg-113 to Gly-118. Pro-131 to Arg-142. Asp-155 to Leu-166.
739143	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 804 as residues: Ala-1 to Gly-14. Glu-21 to Gly-27. Asp-54 to Lys-59. Lys-64 to Glu-71. Gln-92 to Leu-97. Asn-114 to His-120. Leu-135 to Asp-142. Glu-149 to Ser-154. Ser-256 to Thr-261. Asp-290 to Lys-301. Glu-315 to Gln-323. Lys-331 to Asn-342. Arg-346 to Met-361.
742329	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 805 as residues: Arg-7 to Ala-13. Gln-21 to Ser-27. Gln-68 to Gly-73. Pro-75 to Val-88.
745481	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 807 as residues: Asn-1 to Lys-14. Arg-32 to His-39. Asn-46 to Gly-51.
753731	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 809 as residues: Arg-22 to Ser-39. Val-42 to Thr-54. Gln-61 to His-69.
754383	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 810 as residues: Ala-2 to Gly-12.
756749	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 811 as residues: His-1 to Thr-11. Thr-13 to Ser-18. Gly-25 to Gly-30. Pro-63 to Pro-69. Glu-84 to Tyr-101. Asn-110 to Ala-140.
757980	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 812 as residues: Phe-9 to His-21.
764818	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 813 as residues: Pro-12 to Trp-17. Asn-22 to Ala-37. Arg-45 to Gly-54. Asp-72 to Thr-95. Pro-97 to Glu-116. Gly-137 to Lys-151. Glu-164 to Asp-171. Ser-175 to Gly-185. Glu-187 to Gly-213. Lys-270 to Glu-276. Leu-281 to Lys-286. Asp-314 to Gly-321. Glu-324 to Glu-331. Val-333 to Arg-340.
765140	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 814 as residues: Thr-15 to Asp-27.
766893	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 815 as residues: Arg-6 to Leu-11. Arg-21 to Tyr-27. Phe-37 to Lys-46. Gly-59 to Gly-64.
771412	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 817 as residues: Pro-1 to His-6. Pro-37 to Arg-47.
772226	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 818 as residues: Phe-16 to Arg-30. Glu-35 to Trp-58. Lys-60 to Gln-68. Pro-80 to Tyr-85.
773057	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 819 as residues: Gly-37 to Arg-43.
773173	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 820 as residues: Pro-19 to Asn-26.
780154	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 821 as residues: Arg-20 to Ile-31. Pro-34 to Ala-59. Glu-66 to Pro-125. Leu-132 to Lys-137. Lys-155 to Arg-259.
780768	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 822 as residues: Phe-12 to Lys-17.
780779	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 823 as residues: Ser-1 to Ser-11. Gln-64 to Gln-69. Arg-117 to Arg-127.
782394	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 824 as residues: Phe-18 to Gly-24.
783160	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 825 as residues: Lys-35 to Lys-41. Thr-50 to His-56. Thr-110 to Gly-119.
783506	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 826 as residues: Thr-3 to Thr-9.
792139	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 830 as residues: Arg-1 to Thr-13. Arg-21 to Pro-30. Ser-70 to Arg-79. Asp-89 to Arg-101.

805715	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 832 as residues: Met-7 to Ala-17, Arg-26 to Lys-32, Lys-47 to Lys-52, Asn-67 to Asn-72, Val-77 to Tyr-82, Pro-101 to Arg-107, Arg-137 to Arg-146, Ser-168 to Thr-173, Asp-189 to Lys-199.
811111	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 833 as residues: His-24 to Asn-31.
811113	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 834 as residues: Gln-1 to Ala-9, Cys-56 to Gly-61, Trp-105 to Thr-110, Arg-150 to Thr-155, Leu-189 to Lys-195.
823902	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 835 as residues: Thr-18 to Glu-23.
826518	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 836 as residues: Ile-20 to Lys-26, Cys-39 to Arg-46.
826704	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 837 as residues: His-14 to Phe-20, Glu-70 to Leu-83.
828180	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 840 as residues: Glu-38 to Arg-52, Ser-56 to Val-62.
828658	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 842 as residues: Asp-1 to Pro-12, Gly-59 to Lys-64, Asp-70 to Leu-76, Pro-160 to Pro-166, Thr-174 to Asn-179.
828919	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 843 as residues: Thr-49 to Val-54, Leu-83 to Lys-91, Gly-121 to Thr-130, Asp-165 to Glu-172, Thr-180 to Gly-188.
830208	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 846 as residues: Lys-49 to Asn-56, Glu-61 to Ala-67.
830248	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 847 as residues: Pro-17 to Asp-36, Pro-102 to Glu-108, Pro-122 to Lys-128, His-150 to Gly-155, Asn-162 to Tyr-168, Pro-186 to Gln-193, Ser-205 to Pro-211, Gln-305 to Gly-317.
830275	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 848 as residues: Ser-16 to Glu-22, Asn-45 to Ser-50, Thr-121 to Gly-136, Lys-150 to Arg-157, Ser-175 to Cys-181, Gly-198 to Ser-203.
830286	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 849 as residues: His-11 to Pro-18, Thr-241 to Thr-258, Ala-352 to Ala-365.
830347	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 850 as residues: Asp-33 to Ala-39.
830348	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 851 as residues: Gln-5 to Arg-15, Ile-96 to Asn-101, Asp-122 to Gly-128.
830364	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 852 as residues: Val-76 to Asn-82, Lys-87 to Tyr-94, Glu-118 to Gln-125, Pro-140 to Ile-145, Gly-149 to Pro-173, Ala-215 to Lys-222, Lys-230 to Gly-235, Pro-250 to Asn-256, Ser-302 to Arg-307, Ser-321 to Glu-332.
830394	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 853 as residues: Thr-37 to Thr-44, Leu-57 to Ser-63, Ser-74 to Lys-86, Gln-107 to Leu-112, Lys-140 to Ala-145, Asp-154 to Ser-163.
830412	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 855 as residues: His-65 to Gly-74, Asp-85 to Ser-97, Leu-133 to Glu-138, Glu-144 to Asp-153, Arg-170 to Ser-175, Gly-184 to Arg-189, Gln-202 to Tyr-208.
830464	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 857 as residues: Val-3 to Val-11, Gln-16 to Gln-27, Glu-41 to Asp-51.
830471	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 858 as residues: Glu-10 to His-22, Ser-37 to Lys-45.
830477	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 859 as residues: Lys-1 to Cys-13, Thr-32 to Cys-37, Ser-44 to Glu-50, Glu-57 to Asn-64, Glu-85 to Glu-93, Ala-129 to Ser-139, Gln-157 to Thr-185, Gln-199 to Gly-215, Ile-241 to Leu-247, Asp-254 to Leu-263, Gln-265 to Gln-270, Glu-298 to Gln-309, Glu-316 to Ala-321, Leu-325 to Glu-334, Glu-340 to Ser-345, Leu-348 to His-367, Lys-384 to Arg-391.

	Leu-409 to Asn-417, Arg-431 to Arg-437, Phe-441 to Leu-448, Ala-456 to Glu-484, Lys-509 to Val-519, Glu-521 to Asp-528, Asp-546 to Phe-553, Glu-558 to Phe-567, Pro-573 to Thr-588.
830500	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 860 as residues: Gln-27 to Gly-34.
830509	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 861 as residues: Pro-2 to Asp-7, Gln-13 to Gln-29, Pro-35 to Trp-41.
830528	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 862 as residues: Gln-1 to Arg-12, Asp-22 to Pro-44, Lys-52 to Asp-62, Pro-68 to Lys-93, Pro-99 to Pro-129, Ala-138 to Ser-150, Lys-156 to Val-194, Ile-197 to Glu-210, Ala-213 to Ala-287, Leu-289 to Lys-327, Lys-330 to Gly-340, Asp-344 to Gln-360, Ile-396 to Thr-401, Lys-409 to Asp-418, Met-450 to Ala-460, Glu-468 to Gly-475.
830542	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 863 as residues: Val-1 to Gly-10, Arg-24 to Asp-36, Leu-225 to Trp-231, Val-249 to Met-258, Glu-262 to Thr-269, Val-279 to Gly-284, Asp-307 to Asn-313, Arg-411 to Lys-416.
830564	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 864 as residues: Trp-103 to Glu-113, Lys-118 to Tyr-125.
830611	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 865 as residues: Glu-51 to Ser-57, Arg-128 to Ala-133.
830620	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 867 as residues: Lys-54 to Arg-59, Arg-66 to Arg-71.
830630	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 868 as residues: Pro-12 to Gly-17.
830654	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 869 as residues: Leu-1 to Asp-6.
830660	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 870 as residues: Lys-111 to Trp-116, Glu-139 to Gly-148, Arg-182 to Ser-189.
830704	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 872 as residues: Asn-1 to Glu-8, Ala-38 to Gly-46, Gln-58 to Asp-71, Ala-75 to Cys-103, Met-106 to Ala-140, Gln-153 to Ile-159.
830765	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 873 as residues: Ser-19 to Thr-26, Pro-47 to Thr-59.
830778	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 874 as residues: Asp-35 to Gly-40, Glu-104 to Glu-109, Ser-226 to Tyr-231.
830784	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 875 as residues: Pro-34 to Leu-41.
830800	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 876 as residues: Ser-16 to Lys-24, Gly-91 to Thr-96.
830821	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 877 as residues: Leu-2 to Thr-8, Asp-15 to Gly-26, Phe-64 to Ser-70, Pro-77 to Trp-82, Pro-85 to Lys-90.
830849	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 878 as residues: Leu-2 to Ser-18, Gly-31 to Ser-40, Asn-56 to Thr-86, Asp-114 to Arg-120.
830903	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 879 as residues: Thr-21 to Thr-33.
830913	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 880 as residues: Glv-48 to Pro-53, Gln-66 to Pro-74, Thr-151 to Gly-156, Asn-292 to Asn-297.
830920	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 881 as residues: Asp-15 to Ser-25, Ser-33 to Val-38, Lys-181 to Phe-187.
830938	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 882 as residues: Thr-65 to Asp-70, Leu-89 to Ala-95.
831014	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 884 as residues: Ala-2 to Gln-11, Glu-71 to Leu-78, Leu-89 to Trp-98, Ser-163 to Ala-170, Glu-261 to Asp-269, Phe-286 to Val-292.
831026	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 885 as residues: Lys-41 to Glv-46, Tyr-64 to Phe-75.

831055	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 887 as residues: Trp-37 to His-50, Lys-108 to Phe-114, Lys-131 to Thr-137, Arg-351 to Ser-356, Pro-363 to Cys-369, Glu-390 to Asp-397.
831057	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 888 as residues: Arg-1 to Gly-14, Thr-19 to Gly-25, Ala-31 to Ala-41, Glu-53 to Ile-62, Val-66 to Glu-75, Ser-103 to Asp-113, Ala-135 to Asp-140.
831062	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 889 as residues: Scr-24 to Ala-31.
831117	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 890 as residues: Lys-50 to Tyr-55.
831122	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 891 as residues: Phe-8 to Gly-14, Arg-58 to Gly-68, Lys-107 to Ser-131, Gln-151 to Val-160, Lys-180 to Lys-186, Lys-211 to Thr-223.
831132	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 893 as residues: Gly-1 to Ser-16.
831152	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 894 as residues: Ser-8 to Arg-13, Lys-59 to Ala-65, Glu-71 to Glu-86, Leu-98 to His-108, Arg-118 to Ile-126, His-138 to Ala-145, Pro-148 to Tyr-156, Pro-170 to Ala-175, Val-187 to Lys-194, Glu-206 to Val-217, Gly-221 to Ser-226, Asp-250 to Lys-255.
831157	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 895 as residues: Val-1 to Asn-11, Glu-13 to Gly-25, Scr-31 to Ala-49, Arg-61 to Gly-66, Ala-84 to Ala-90.
831160	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 896 as residues: His-1 to Ala-7, Asp-43 to Lys-52, Tyr-98 to Gly-103, Glu-118 to Leu-125, Phe-183 to Tyr-195, Gln-209 to Arg-220, Ile-257 to Gly-262, Glu-278 to Thr-284, Ile-309 to Pro-314, Leu-339 to Asp-347, Ala-358 to Gln-388, Gln-401 to Leu-414, Glu-425 to Ala-440, Ala-448 to Glu-453, Ile-460 to Gln-465, Glu-482 to Glu-492, Ala-498 to Glu-511, Pro-520 to Val-526, Gly-556 to Gln-577, Leu-587 to His-598, Glu-605 to Asp-630.
831197	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 898 as residues: Ser-28 to Leu-39, Phe-48 to Phe-55, Pro-60 to Gln-66, Arg-73 to Thr-78.
831217	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 899 as residues: Asp-52 to Val-63, Asn-75 to Glu-83.
831248	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 901 as residues: Pro-24 to Gly-34, Lys-108 to Arg-118.
831369	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 903 as residues: Ala-1 to Gly-8.
831371	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 904 as residues: Arg-39 to Ser-44, Arg-66 to Arg-76.
831373	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 905 as residues: Gly-7 to Ser-13, Gln-40 to Trp-45, Lys-109 to Gly-116, Gly-134 to Arg-141, Arg-149 to Arg-164, Arg-174 to Phe-181, Lys-202 to Lys-210, Glu-263 to Leu-272, Pro-274 to Leu-280, Glu-289 to Glu-296, Pro-334 to His-341, Tyr-413 to Pro-426, Glu-432 to Lys-449.
831387	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 906 as residues: Tyr-21 to Leu-28, Cys-51 to Phe-72, Ser-107 to Leu-113, Leu-125 to Leu-134, Ser-142 to Ala-152, His-159 to Tyr-164, Arg-276 to Val-290.
831410	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 907 as residues: Arg-7 to Lys-13, Pro-28 to Cys-34, Gly-100 to Asn-109, Cys-155 to Arg-162.
831448	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 908 as residues: Ala-10 to Cys-20, Tyr-36 to Lys-41, Asp-68 to Ala-75, Ala-84 to Arg-89, Glu-112 to Ser-119.
831450	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 909 as residues: Pro-23 to Gly-28, Thr-52 to Pro-63.
831472	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 910 as residues: Scr-16 to Ala-26.

831473	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 911 as residues: Arg-37 to Gln-42, Asn-59 to Asn-65, Asn-109 to Val-121, Arg-191 to Glu-199, Lys-205 to Ile-214.
831474	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 912 as residues: Glu-1 to Leu-8, Ser-50 to Arg-56, Thr-61 to Arg-66, Val-69 to Arg-82.
831494	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 913 as residues: Arg-21 to Ser-27, Arg-77 to Asp-82, Glu-116 to Ile-134, Ser-139 to Ser-162, Leu-167 to Gly-190, Cys-192 to Gly-205.
831506	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 914 as residues: Val-6 to Tyr-12, Lys-77 to Ala-82, Ser-102 to Arg-108, Ser-145 to Ser-151.
831533	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 915 as residues: Thr-9 to Cys-16, Arg-52 to Tyr-57, Ser-61 to Ser-69.
831539	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 916 as residues: Thr-32 to Arg-39, Cys-44 to Arg-60, Lys-65 to Gln-70, Gly-78 to Ile-86, Lys-126 to Thr-134, Leu-140 to Glu-148.
831556	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 917 as residues: Gly-45 to Asp-52.
831598	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 919 as residues: Asn-1 to Val-6, Phe-76 to Tyr-83, Gly-129 to Gln-135, Thr-145 to Asp-153, Pro-213 to Gln-220, Thr-230 to Asn-236, Lys-242 to Ala-248.
831608	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 920 as residues: Thr-23 to Pro-34, Glu-39 to Asp-83, Asn-89 to Lys-99, Asp-118 to Asp-128, Asn-135 to Glu-150, Glu-153 to Gly-168, Gly-181 to Thr-187, Arg-200 to Asp-205, Arg-273 to Ile-279, Thr-295 to Asp-300, Thr-316 to Cys-321.
831613	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 921 as residues: Pro-1 to Glu-7, Arg-9 to Phe-15, Thr-27 to Gly-34.
831655	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 926 as residues: Tyr-31 to Gln-38.
831708	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 927 as residues: Glu-22 to Ile-27, Gly-43 to Gly-49, His-83 to Arg-105.
831741	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 929 as residues: Asp-22 to Asp-27, Pro-64 to Gln-74, Ser-126 to Gly-131, Lys-134 to Arg-143, Arg-150 to Gly-162, Gln-180 to Tyr-196, Asp-209 to Leu-224, Gly-233 to Gly-241, Pro-246 to Arg-251.
831754	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 930 as residues: Arg-40 to Glu-50, Gly-57 to Gly-68, Phe-72 to Tyr-79.
831760	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 931 as residues: His-24 to Asp-39.
831780	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 932 as residues: Arg-92 to Thr-101.
831796	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 933 as residues: Pro-1 to Ser-8.
831800	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 934 as residues: Asp-1 to Ser-6, Glu-16 to Ser-26, Lys-66 to Pro-76, Leu-93 to Arg-99, Val-153 to Lys-164, Glu-177 to Asp-183, Ser-188 to Leu-193, Arg-210 to Ser-220, Thr-229 to Ser-244, Pro-283 to Phe-297.
831813	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 937 as residues: Pro-20 to Ala-30.
831830	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 938 as residues: Arg-12 to Lys-17, Gln-51 to Phe-60, Asp-97 to Trp-102, Glu-132 to Cys-137, Asp-160 to Leu-168, Glu-210 to Gln-219, Lys-302 to Pro-308, Phe-416 to Asp-421, Leu-444 to Leu-449, Val-457 to Asn-464, Leu-466 to Trp-472, Ile-474 to Trp-480, Ser-527 to Ser-533, Pro-558 to Phe-565, Ile-578 to Trp-584, Asp-614 to Asp-627, Asn-698 to Asp-710, Pro-738 to Ser-744.
831860	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 939 as residues: Pro-19 to Tyr-25.

831896	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 941 as residues: Ser-18 to Phe-30, Leu-34 to Asn-41, Ala-48 to Tyr-56, Leu-103 to Ala-110, Asp-124 to Val-130, Ile-141 to Leu-150, Leu-188 to Ser-196, Glu-229 to Asn-238, Thr-248 to Cys-259.
831928	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 942 as residues: Asn-55 to Asp-60.
831949	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 943 as residues: Arg-1 to Glu-9, Glu-19 to Arg-32, Ala-77 to Thr-90, Thr-95 to Thr-104, Lys-106 to Ser-119, Leu-136 to Arg-141, Tyr-165 to Asn-174.
831950	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 944 as residues: Ser-18 to Glu-26, Phe-93 to Arg-102, Leu-137 to Gln-143, Pro-148 to Gly-157.
831975	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 946 as residues: His-41 to Thr-48.
832047	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 948 as residues: Arg-57 to Glu-62, Pro-73 to Gly-80.
832078	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 949 as residues: Pro-14 to Leu-21, Cys-34 to Gly-39.
832100	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 950 as residues: Tyr-37 to Val-45.
832104	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 951 as residues: Thr-1 to Ser-6, Arg-14 to Cys-20.
832279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 954 as residues: Ser-28 to Pro-34, Pro-134 to Ser-139, Gln-178 to Gly-183, Thr-193 to Gly-198, His-244 to Gly-257, Asp-263 to Tyr-273, Lys-337 to Arg-347, Pro-366 to Lys-372, Ala-382 to Asp-387.
832317	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 955 as residues: Thr-32 to Gln-39, Asn-58 to Trp-71, Glu-96 to Trp-108, Cys-126 to Gly-133.
832364	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 957 as residues: Glu-2 to Met-9, Asp-17 to Asn-22, Leu-27 to Val-35.
832428	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 960 as residues: Arg-35 to Gly-41.
832485	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 961 as residues: Ser-121 to Cys-127.
832494	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 962 as residues: Ser-10 to Leu-28, Ser-31 to Asp-40, Ser-55 to Thr-62, Thr-94 to Asn-102, Asp-124 to Phe-135, Asn-175 to Lys-193, Glu-238 to Leu-243, Val-250 to Ala-259, Lys-291 to Asn-308, Ser-318 to Gly-327, Lys-335 to Asp-346, Tyr-404 to Ile-410, Gln-420 to Gln-430, Thr-476 to Phe-482, Pro-536 to Val-561, Tyr-563 to Leu-568.
832512	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 963 as residues: Arg-1 to Ala-7, Leu-9 to Ser-24, Glu-32 to Asp-43, Glu-71 to Glu-86, Val-92 to Ile-104, Asp-143 to Ser-154, Lys-190 to Glu-202, Glu-218 to Lys-241.
832515	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 964 as residues: Glu-3 to Gly-12, Arg-20 to Gln-30, Leu-34 to Gln-39, Asp-51 to Arg-58, Gln-69 to Val-77, Gly-105 to Lys-117, Cys-123 to Phe-132.
832526	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 965 as residues: Pro-15 to Asn-25, Glu-48 to Phe-59.
832575	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 966 as residues: Thr-24 to Arg-29, Ala-55 to Tyr-60, Tyr-77 to Asp-89, Leu-108 to Gly-115, Thr-142 to Gly-149.
832576	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 967 as residues: Arg-1 to Leu-11, Pro-21 to Gly-28, Pro-37 to His-47, Lys-79 to Gln-88, Pro-108 to Gly-116, Pro-179 to Thr-188, Arg-207 to Asn-213.
832634	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 969 as residues: Leu-2 to Ser-12, Pro-125 to Asp-133.
832728	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 970 as residues: Gln-16 to Gly-32, Leu-100 to Gly-106, Gly-118 to Lys-132, Pro-156 to Leu-

	162.
833395	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 972 as residues: Ser-3 to Gly-9.
834326	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 973 as residues: Ser-1 to Trp-19, Asn-148 to Leu-153, Tyr-235 to Trp-244.
834944	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 975 as residues: Glu-42 to Gln-51, Pro-115 to Asp-120, Arg-127 to Gly-133, Gln-199 to Gln-211.
835104	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 977 as residues: Thr-1 to Arg-14, Val-18 to Pro-23, Thr-37 to Met-44, Gln-51 to Leu-57.
835332	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 978 as residues: Thr-1 to Glu-13, Arg-135 to Asp-142, Thr-150 to Gln-155, Cys-173 to Cys-183, Cys-203 to Asp-214.
835487	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 979 as residues: Ala-13 to Arg-22, Pro-43 to Glu-57, Ala-73 to Pro-90, Arg-102 to Ser-109, Pro-114 to Gly-122, Arg-127 to Arg-138, Glu-153 to Gly-158, Pro-165 to Pro-171, Gly-185 to Arg-190, Pro-211 to Pro-216, Glu-231 to Asn-261, Ala-280 to Pro-291, Pro-303 to Gly-311, Arg-313 to Gly-326, Ala-358 to Ala-364, Pro-369 to Gly-377, Pro-390 to Gly-407, Tyr-420 to Tyr-441, Glu-461 to Thr-470, Pro-479 to Trp-487, Asp-489 to Cys-494, Gln-515 to Lys-532, Ala-572 to Asn-582, Asp-588 to Leu-594, Cys-625 to Trp-632, Tyr-639 to Arg-646.
836182	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 980 as residues: Ala-7 to Thr-17, Arg-31 to Thr-36.
836522	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 981 as residues: Gly-59 to Cys-65.
836789	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 984 as residues: Gly-18 to Gly-25, Glu-59 to Glu-64.
838577	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 985 as residues: Pro-15 to Trp-20, Pro-46 to Gln-57, Glu-68 to Phe-83.
839008	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 987 as residues: Arg-1 to Arg-13, Gln-125 to Glu-131, Asn-137 to Val-142, Gly-183 to Tyr-188, Asn-245 to Ser-251, Gln-302 to Asn-311.
840063	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 988 as residues: Gly-1 to Gly-31.
840533	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 989 as residues: Thr-16 to Pro-23, Pro-39 to Trp-48, Arg-50 to Lys-55, Glu-73 to Gly-79.
840669	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 990 as residues: Met-27 to Gln-33, Gln-49 to Gly-56, Thr-63 to Leu-70, Thr-115 to Arg-127, Pro-174 to Asn-184.
841140	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 991 as residues: Arg-17 to Phe-24, Pro-113 to Gly-121, Thr-235 to Met-240.
841386	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 992 as residues: Val-58 to Met-66, Pro-134 to Lys-143, Tyr-163 to Ala-170, Val-178 to Lys-187, Pro-207 to Gly-212.
841900	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 996 as residues: Ile-2 to Phe-12.
842054	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 997 as residues: Asp-27 to Trp-32, Pro-89 to Glu-99, Arg-112 to Lys-123.
843061	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 998 as residues: Leu-3 to Gly-18, His-36 to His-57, Lys-136 to Leu-145, Gly-174 to Trp-184, Lys-188 to Tyr-196, Lys-204 to Asp-211, Pro-293 to Ser-305, Glu-321 to Asp-333, Gly-342 to Lys-348, Ala-371 to Asp-377, Asp-439 to Leu-449, Ala-521 to Gly-529, Tyr-583 to Trp-599, Asn-639 to Ser-644, Leu-738 to Leu-745.
843544	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 999 as residues: Tyr-11 to Phe-18, Ser-34 to Lys-43.
844092	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1000 as

	residues: Gln-1 to Lys-6, Glu-30 to Glu-37, Glu-40 to Thr-53.
844270	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1001 as residues: Thr-10 to Gly-20, Pro-44 to Thr-50.
844604	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1002 as residues: Gly-8 to Phe-20, Pro-23 to Arg-43, Asp-62 to Asp-67, Pro-73 to Asn-80, Val-83 to Phe-95, Glu-103 to Ile-109, Tyr-120 to Ala-125, Thr-176 to Thr-183, Pro-200 to Pro-214, Pro-232 to Met-240, Gln-248 to Asp-292, Arg-297 to Ser-310, Pro-320 to Glu-332, Glu-347 to Ser-390, Ala-392 to Pro-404, Pro-425 to Gly-435, Pro-438 to Gly-443, Gly-467 to Pro-480, Pro-486 to Pro-499, Pro-506 to Met-512, Pro-572 to Glu-580, Arg-592 to Gly-597, Ala-601 to Ser-610, Ala-618 to Pro-623.
844685	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1003 as residues: Ser-14 to Ser-19, Pro-25 to Gly-32, Asn-98 to Lys-108.
844855	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1004 as residues: Ala-9 to Ser-15, Pro-21 to Arg-26.
845101	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1005 as residues: Ala-2 to Gly-13, Pro-31 to Pro-42, Gln-89 to Tyr-95, Gln-169 to Leu-189.
845141	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1006 as residues: Gly-13 to Met-26, Arg-34 to Gly-39, Ile-60 to Ser-80, Ala-85 to Thr-98.
845220	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1007 as residues: Pro-14 to Gly-24, Glu-33 to Ala-39, Asp-145 to Pro-168, Ala-238 to Arg-250, Pro-258 to Phe-269, Arg-285 to Pro-290, Ala-340 to Cys-364.
845434	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1008 as residues: Ala-1 to Glu-7, Gln-29 to Phe-34, Gly-67 to Ala-75, Gln-78 to Leu-83, Asn-96 to Ile-109, Thr-144 to Trp-151.
845510	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1009 as residues: Arg-79 to Leu-86, Met-114 to Asp-122, Leu-129 to Leu-134, Gln-145 to Arg-152.
845600	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1010 as residues: Ala-22 to Phe-28.
845882	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1011 as residues: Ala-1 to Gly-7, Arg-29 to Lys-35, Lys-72 to Ala-79, Leu-94 to Val-101, Gly-137 to Asn-142, Arg-145 to Leu-150, Gly-180 to Lys-187, Glu-194 to Gly-208, Arg-257 to Ser-267, Ser-278 to Asp-290, Gly-312 to Ser-319, Leu-338 to Lys-351, Tyr-358 to Ser-363.
846007	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1012 as residues: Tyr-16 to Ala-24, Arg-59 to Ser-66, Thr-78 to Glu-83, Glu-90 to Ser-103, Gln-108 to Thr-113, Ser-115 to Cys-124.
HCRNG17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1016 as residues: Pro-16 to Asp-21.
HWMFG64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1017 as residues: Ser-70 to Asp-76, Lys-87 to Leu-95.
HAGCZ94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1018 as residues: Val-3 to Lys-9.
HBJEJ74R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1019 as residues: Pro-1 to Asp-8.
HUTHM43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1021 as residues: Pro-7 to Arg-15.
HLTGU75R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1022 as residues: Ser-1 to Gly-11.
HWLKF77R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1023 as residues: Leu-10 to Asn-28.
HWLGX29R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1027 as residues: Val-3 to Ile-10, Pro-34 to Gln-40.
HWMFZ29R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1028 as residues: Leu-7 to Leu-13.
H6EEP19R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1030 as

	residues: Ala-1 to Trp-8, Lys-10 to Asp-27.
HJMAM83R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1031 as residues: Ser-1 to Val-11, Glu-19 to Ala-29, Asp-52 to Ala-68, Gly-78 to Lys-94.
HAGHF58R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1032 as residues: Lys-1 to Val-7.
HDPHG48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1033 as residues: Gly-24 to Lys-34.
HCDMC32R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1038 as residues: Pro-2 to Arg-17, Lys-36 to Pro-47, Phe-61 to Trp-68, Gln-72 to Ala-86.
HTEQO80R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1040 as residues: Gly-1 to Val-15, Pro-17 to Pro-23, Leu-32 to Met-41, Lys-102 to His-109.
H2LAR08R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1043 as residues: Asn-58 to Gly-64.
HWMFN58R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1046 as residues: Glu-6 to Asn-14, Arg-22 to Asp-31, Gly-49 to Thr-56.
HUFBP63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1049 as residues: Pro-1 to Gln-8, Thr-57 to Gly-64, Arg-69 to Arg-74, Gly-80 to Asp-91, Asp-105 to Gln-110, Arg-130 to Tyr-148.
HUFBN90R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1050 as residues: Glu-34 to Ala-40, Arg-111 to Ala-116.
HFKHD61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1054 as residues: Arg-11 to Gly-38, Arg-44 to Glu-50, Gln-53 to Lys-67.
HTXNL13R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1057 as residues: Ser-48 to Arg-57, Glu-89 to Pro-95, Ser-102 to Asn-107.
H2LAK62R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1059 as residues: Pro-20 to Ser-25.
HATAR77R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1061 as residues: Gly-2 to Arg-16.
HWMEH18R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1066 as residues: Gln-61 to Ser-67.
HCNDP66R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1068 as residues: Leu-8 to Arg-15, Gln-46 to Pro-54.
HCRMK82R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1069 as residues: Ser-32 to Arg-38, Ala-72 to Lys-79, Arg-103 to Phe-111.
HSSGC52R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1075 as residues: Gly-1 to Pro-6, Arg-25 to Ile-30.
HCYBN49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1076 as residues: Gly-16 to Gly-21, Ile-99 to Gln-109.
HWMGB90R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1077 as residues: Gly-1 to Ala-7, Asp-17 to Arg-27, Glu-32 to Leu-40.
HTEAW21R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1078 as residues: Glu-1 to Gly-6, Gln-19 to Leu-37.
H2LAQ68R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1082 as residues: Val-2 to Trp-10, Leu-25 to Lys-33.
HBAAD60R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1087 as residues: Pro-1 to Lys-32.
HCROA35R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1088 as residues: Gly-6 to Lys-12.
HCROM64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1089 as residues: Asn-1 to Arg-7.
HKBAG82R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1091 as residues: Pro-9 to Gly-28.
HUTSB76R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1092 as residues: Lys-1 to Ser-17.
HWLJS67R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1093 as residues: Gln-3 to Lys-18, Gln-44 to Glu-49.

HTGAZ53R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1098 as residues: Ser-1 to Ala-16, Gln-36 to Thr-48.
HWLLL51R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1100 as residues: Gln-6 to Gly-18.
HWLJZ72R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1103 as residues: Ile-1 to Ser-19.
HWMFG06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1104 as residues: Arg-1 to Lys-14, Gln-40 to Glu-45, Arg-65 to Arg-80.
HPRTO65R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1105 as residues: Thr-12 to Thr-17, Cys-35 to Ser-40.
HUFDC01R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1106 as residues: Pro-11 to Glu-26.
HWLHY44R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1107 as residues: Pro-14 to Gln-24, Cys-34 to Leu-39, Thr-72 to Val-77, Glu-94 to Thr-99, Asp-101 to Met-107, Lys-109 to Pro-116.
HWLGR92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1108 as residues: Pro-17 to Gly-22.
HCNCQ71R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1109 as residues: Glu-22 to Leu-30.
HWLEN11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1111 as residues: Pro-6 to Lys-21, Ala-26 to Val-34, Lys-37 to Ser-46.
HWLEH56R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1116 as residues: Thr-23 to Ala-28, Asn-88 to Trp-98, Cys-114 to Asp-131.
H2LAD26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1117 as residues: Pro-20 to Gly-31.
H2LAK66R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1125 as residues: Pro-33 to Leu-39, Glu-54 to Val-59, Gly-69 to Ser-76.
HSDKC65R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1126 as residues: Asn-32 to Pro-39, Pro-41 to Pro-49.
H2LAK52R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1127 as residues: Pro-20 to Ala-28.
HKAEG12R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1128 as residues: Asp-47 to Lys-52.
HKADP43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1129 as residues: Pro-7 to Pro-15, Arg-35 to Val-44.
HUSJE17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1131 as residues: Pro-26 to Gln-32.
HHBEF06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1133 as residues: Pro-1 to Gly-6.
HISCW28R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1134 as residues: Pro-26 to Gln-32.
HPIAK29R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1137 as residues: Thr-1 to Tyr-7.
HUFAR71R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1138 as residues: Pro-26 to Gln-32.
HOECI21R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1141 as residues: Asn-11 to Pro-20, Pro-22 to Thr-30, Glu-49 to Glu-70, Ser-84 to Thr-96, Thr-108 to Thr-113.
HMCAR63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1143 as residues: Ala-1 to Gly-9, Lys-41 to Glu-47, Asn-65 to Gly-70, Glu-85 to Asp-93, Glu-103 to Tyr-109.
HAICY55R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1152 as residues: Glu-2 to His-9.
HWLIA38R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1153 as residues: Arg-60 to Gly-74, Ser-80 to Ile-88, Leu-92 to Ser-98.
HBXCL69R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1154 as

	residues: Ser-2 to Cys-8, Pro-10 to Leu-17.
H2LAP90R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1155 as residues: Thr-3 to Gln-9, Asn-11 to Pro-19, Gln-35 to Glu-42.
HTELE03R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1157 as residues: Asp-1 to Gln-9, Asn-11 to Arg-16, Cys-28 to Ser-44, Gln-50 to Gln-56.
HJMBN86R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1158 as residues: Ser-31 to Glu-47.
HSKJC32R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1159 as residues: Gln-151 to Glu-158, Glu-168 to Pro-173, Ser-188 to Ile-195.
HAOAG76R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1161 as residues: Gly-1 to Ala-14.
HCIAD45R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1162 as residues: Pro-1 to Lys-23, Pro-43 to Leu-49.
H2MAC82R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1163 as residues: Lys-54 to Lys-59.
H2LAJ41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1164 as residues: Met-20 to Val-36, Ser-82 to Lys-93, Pro-101 to Arg-106.
HBJFH33R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1166 as residues: Gly-10 to Tyr-26, Asn-29 to Leu-37, Thr-52 to His-59.
HISDV92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1167 as residues: Pro-3 to Ser-8, Asn-48 to Tyr-54.
HE9QB35R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1169 as residues: Gly-1 to Asp-6, Pro-20 to Gln-33, Tyr-46 to Arg-52, Asn-72 to Lys-85, Gln-91 to Ala-110.
HDABQ50R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1170 as residues: Ser-9 to Lys-17, Lys-41 to Arg-46.
HTPAC28R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1176 as residues: Lys-10 to Thr-15, Thr-17 to Leu-23.
HMCGN07R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1177 as residues: Asn-88 to Ser-98, Pro-123 to Val-129.
HBMVM66R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1180 as residues: Ser-2 to Gly-7, Arg-10 to Phe-24, Ala-36 to Arg-41.
HEPNA09R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1186 as residues: Ser-1 to Pro-6.
HCNDR62R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1190 as residues: Pro-14 to Ser-21.
HNJBF13R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1191 as residues: Asp-18 to Asp-28.
HLYCD69R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1192 as residues: Gly-90 to Thr-109.
HWCAA53R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1194 as residues: Ser-22 to Gly-28, Glu-37 to Ile-45, Val-67 to Arg-85, Asn-91 to Trp-99.
HFVGP11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1198 as residues: Ala-4 to Asn-13.
HWLQH07R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1199 as residues: Lys-1 to Lys-25.
HWLKH07R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1201 as residues: Pro-49 to Asp-58.
HAPQC14R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1202 as residues: Lys-1 to Met-8.
HSODB48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1203 as residues: Ser-24 to Gly-31, Ala-37 to Ser-44, Pro-57 to Ser-64, Pro-97 to Gly-104.
HBEAC75R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1204 as residues: Pro-1 to Arg-9.
HBGMJ24R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1205 as residues: Tyr-11 to Val-17, Thr-30 to Phe-48, Gln-150 to Thr-155.

HBJEN94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1206 as residues: Gln-1 to Asn-6.
HLQGB87R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1213 as residues: Lys-2 to Ser-7.
HAOAC69R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1215 as residues: Ser-2 to Arg-10.
HWLEQ08R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1216 as residues: Glu-21 to His-31.
HKAAV70R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1217 as residues: Gly-6 to Thr-93, Glu-95 to Glu-104, Asp-117 to Asp-125.
HNFJE41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1221 as residues: Arg-15 to His-21, Pro-48 to Ala-58, Asn-61 to Leu-66, Val-92 to Thr-110, Pro-114 to Thr-120.
HCRMW41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1224 as residues: Phe-14 to Asn-19.
HOVAX78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1225 as residues: Gly-1 to Thr-8.
HWAEH57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1226 as residues: Ser-54 to Tyr-60, Gln-65 to Pro-72, Thr-81 to Gly-92.
HAHEK76R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1230 as residues: Cys-20 to Cys-28.
HOSCG81R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1232 as residues: Thr-8 to Asn-13.
HTFMD43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1233 as residues: Lys-44 to Ile-52, Arg-57 to Lys-77.
H2LAR73R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1235 as residues: Pro-20 to Arg-27, Asn-47 to Lys-53, Asp-116 to Asn-123, Glu-145 to Gly-154.
HWHPK71R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1238 as residues: Asp-15 to His-24, Pro-27 to Leu-39.
HWBBJ39R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1239 as residues: His-1 to Lys-6.
HSODD94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1241 as residues: Gly-7 to Glu-15, Gly-29 to Lys-41, Pro-43 to Ser-52, Pro-68 to His-73.
HMIAG25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1242 as residues: Arg-19 to Ser-41, Pro-43 to Glu-54, Ser-59 to Gly-74.
HCNDW17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1244 as residues: Lys-7 to Lys-15, Thr-54 to Asn-59.
HWLEY08R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1245 as residues: Glu-9 to Arg-14, Thr-19 to Arg-27, Asp-48 to Ile-57, Gln-63 to Leu-75, Cys-89 to Thr-104, Gly-106 to Pro-113.
HULFN68R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1246 as residues: Ser-1 to Cys-16, Lys-18 to Gly-23, Pro-31 to Tyr-37, Gly-53 to Pro-58.
HTEJJ32R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1249 as residues: Ser-17 to Cys-23, Gln-42 to Leu-51, Ser-68 to Asp-73.
H2CBS58R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1251 as residues: Ser-82 to Phe-88, Lys-110 to Gly-118.
H2LAB77R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1252 as residues: Met-13 to Asp-18, Glu-23 to Ser-43, Glu-45 to Gly-54.
HWAFP88R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1254 as residues: Arg-8 to Lys-13, Gly-35 to Lys-42, Ala-48 to Lys-54.
HWMEB67R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1256 as residues: Arg-9 to Arg-16.
HKMAA52R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1261 as residues: Gly-2 to Lys-10, Asp-36 to Asn-42.
H2LAB37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1262 as residues: Glu-52 to Thr-59.

H2LAP46R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1263 as residues: Pro-40 to Asn-46, Tyr-71 to Arg-79.
H6BSE61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1264 as residues: Ile-36 to Asp-41, Ala-54 to Pro-63.
HACBS75R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1269 as residues: Arg-20 to Ser-27, Arg-45 to Trp-59.
HACCA48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1270 as residues: Lys-12 to Lys-26.
HACCS19R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1271 as residues: Gly-1 to Gly-10.
HAGGL96R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1273 as residues: Ser-74 to Phe-88.
HAGGT37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1274 as residues: Phe-17 to Pro-22.
HAHDR66R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1275 as residues: Gly-11 to Ala-18.
HAJCL80R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1277 as residues: Asn-22 to Phe-32.
HAQMH45R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1283 as residues: Pro-2 to Tyr-13, Leu-21 to Gly-47, Val-49 to Gly-55, Pro-63 to Glu-78.
HBGCA44R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1290 as residues: Thr-20 to Trp-25, Lys-32 to Leu-40.
HBGFX27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1291 as residues: Ser-1 to Pro-6.
HBGMU38R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1292 as residues: Gln-1 to Phe-8, Thr-34 to Trp-53, Arg-56 to Gly-63, Arg-86 to Cys-102.
HBJED55R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1295 as residues: Arg-6 to Pro-14.
HBMTJ51R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1300 as residues: Cys-8 to Asp-13.
HBWBD78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1302 as residues: Pro-51 to Ala-58.
HCDDQ63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1307 as residues: Gln-1 to Lys-10.
HCFCD01R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1310 as residues: Ser-1 to Thr-6.
HCFCR43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1311 as residues: Arg-10 to Thr-20.
HCHAO92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1313 as residues: Asn-19 to Arg-25.
HCHOH49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1314 as residues: Asn-19 to Asp-30.
HCHPG05R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1315 as residues: Pro-6 to Ser-11.
HCIAD24R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1316 as residues: Lys-1 to Gly-7.
HCNCY51R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1319 as residues: Lys-10 to Arg-16.
HCNCY63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1320 as residues: Gly-1 to Lys-9.
HCNDO71R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1321 as residues: Lys-33 to Ile-42, Arg-51 to Phe-64.
HCQBN22R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1324 as residues: Lys-1 to Asn-11.
HCQCL27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1325 as residues: Gly-7 to His-27.

HCQCL48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1326 as residues: Ala-1 to Thr-13.
HCQDJ42R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1330 as residues: Glu-8 to Asn-13, Arg-16 to Glu-24.
HCRMD77R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1331 as residues: Asn-4 to Asn-10.
HCROJ68R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1339 as residues: Ile-2 to His-8.
HCROM30R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1342 as residues: Glu-1 to Glu-7, Pro-26 to Leu-32, Gly-37 to Gln-44, Thr-84 to Thr-92.
HCROQ34R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1343 as residues: Asn-1 to Asp-11.
HCROZ66R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1345 as residues: Arg-7 to Lys-13.
HCRPC61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1346 as residues: Ala-3 to Gly-8.
HCRPG28R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1347 as residues: Pro-26 to Ser-32.
HCRPN52R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1349 as residues: Ser-24 to Lys-30, Lys-54 to Ser-61.
HDCAA21R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1354 as residues: Phe-6 to Val-12, Ile-15 to Phe-20.
HDDAA85R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1355 as residues: Lys-18 to Lys-24.
HDPGO03R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1356 as residues: Ala-4 to Gln-17.
HDPLB08R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1357 as residues: Pro-2 to Tyr-13, Leu-21 to Ala-36.
HDQEX80R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1359 as residues: Arg-1 to Arg-6, Phe-27 to Arg-32, Pro-37 to Lys-42, Arg-47 to Trp-53, Arg-55 to Ser-61.
HDRMI91R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1360 as residues: Thr-1 to Lys-8.
HE6DJ45R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1364 as residues: Pro-1 to Asn-8.
HE9FH12R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1366 as residues: Asn-12 to Ser-20.
HEAAL59R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1370 as residues: Gln-20 to Asn-25.
HEGAR32R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1371 as residues: Lys-9 to Ser-19.
HEGAR85R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1372 as residues: Ser-16 to His-46, Arg-49 to Thr-58.
HELFE05R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1373 as residues: Tyr-8 to Leu-16.
HEMFI88R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1374 as residues: Pro-6 to Ala-13.
HEMFR18R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1375 as residues: Ala-1 to Ala-10, Pro-12 to Gly-17, Ala-22 to Cys-27, Glu-30 to Arg-35, Pro-43 to Ser-50.
HEONL43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1376 as residues: Arg-1 to Val-10.
HFADM62R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1380 as residues: Lys-6 to Lys-14.
HFATE31R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1381 as residues: Asp-1 to Arg-9, Arg-20 to Arg-26, Glu-33 to Gly-40.

HFCEL77R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1383 as residues: Glu-33 to Ser-48, Ile-54 to Ile-63, Leu-79 to Asp-84.
HFTBI57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1392 as residues: Pro-18 to Ser-23.
HFXGX46R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1394 as residues: Pro-11 to Gln-28.
HHBEW72R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1400 as residues: Pro-20 to Thr-27.
HHERT59R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1401 as residues: Arg-1 to Trp-9.
HJMAH76R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1405 as residues: Cys-10 to Ala-15.
HJMAM56R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1406 as residues: Ala-45 to Asp-60.
HJMAO54R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1407 as residues: Pro-28 to Gln-39, Pro-65 to Cys-80.
HKLSD93R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1409 as residues: Gly-11 to Gly-17.
HLMFH16R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1410 as residues: Gly-1 to Asp-8.
HLQCQ73R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1412 as residues: Glu-1 to Gly-6, Arg-8 to Phe-13.
HLQEF47R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1413 as residues: Leu-8 to Leu-13.
HLQFM50R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1414 as residues: Gly-29 to Asp-34.
HLQGA76R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1416 as residues: Ser-16 to Ser-33.
HLTEV09R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1418 as residues: Arg-9 to Asn-17.
HMACF85R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1421 as residues: Glu-29 to Lys-34, Leu-113 to Gln-120.
HMAIA15R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1422 as residues: Lys-15 to Gln-21, Ile-51 to Gly-57, Lys-72 to Gly-83.
HMCIS54R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1424 as residues: Lys-3 to His-24.
HNHMR05R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1427 as residues: Pro-9 to Gly-20, Thr-26 to Arg-42, Ala-48 to Ser-54.
HNJBB78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1428 as residues: Thr-6 to Lys-13, Leu-48 to Asn-54.
HOCND06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1433 as residues: Pro-2 to Tyr-13, Leu-21 to Ala-35.
HOCND49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1434 as residues: Asn-2 to Gly-12, Ile-14 to Ala-30.
HODFA26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1436 as residues: Glu-1 to His-6, Gly-19 to Asp-29, Leu-44 to Leu-49.
HODHL89R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1437 as residues: Ser-16 to His-46, Arg-49 to Thr-58.
HOEJM67R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1438 as residues: Ser-19 to Lys-25, Asp-29 to Glu-55, Ser-102 to Thr-107.
HOGBN48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1439 as residues: Lys-14 to Arg-19, Asp-25 to Phe-32.
HOUHN53R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1442 as residues: Glu-1 to His-6, Gly-19 to Trp-31.
HPBEE63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1444 as residues: Pro-14 to Gly-20, His-28 to Arg-35.

HPJBE91R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1446 as residues: Ser-15 to Asn-20. Ala-22 to Ile-49. Lys-52 to Val-57. Tyr-71 to Cys-83, Thr-90 to Tyr-95.
HSDZG83R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1454 as residues: Val-17 to Lys-22.
HSICQ60R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1455 as residues: Val-12 to Gly-17.
HSIFA64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1456 as residues: His-17 to Ile-22. Leu-33 to Pro-40.
HSKYE52R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1458 as residues: Pro-2 to Scr-7.
HSODA95R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1460 as residues: Scr-14 to His-44. Arg-47 to Thr-56.
HSSGK43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1462 as residues: Ser-24 to Leu-35. Pro-38 to Ser-45.
HTXFA64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1470 as residues: Thr-1 to Glu-8.
HUSJF91R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1471 as residues: Gly-1 to Gly-6.
HUSJN48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1472 as residues: Ser-16 to Tyr-24.
HUSZN23R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1474 as residues: Ser-16 to Lys-24.
HUTSD20R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1475 as residues: Arg-10 to Asn-20.
HWAFI63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1477 as residues: Pro-15 to Gly-24. Pro-26 to Arg-45.
HWAGZ89R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1478 as residues: Ser-47 to Lys-52.
HWHHM83R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1480 as residues: Leu-1 to Gly-6.
HWLBS90R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1484 as residues: Lys-37 to Asn-44.
HWLEH13R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1486 as residues: Gln-22 to Glu-29.
HWLEJ67R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1487 as residues: Asn-5 to Trp-13.
HWLEM49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1488 as residues: Glu-1 to His-6, Gly-19 to Trp-31.
HWLGM21R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1492 as residues: Glu-1 to His-6, Gly-19 to Trp-31.
HWLGS46R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1494 as residues: Glu-17 to Asn-23, Glu-38 to Gly-49.
HWLGU40R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1495 as residues: His-10 to Pro-15.
HWLGX65R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1496 as residues: Glu-1 to Asn-7.
HWLHD09R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1497 as residues: Pro-6 to Ala-37, Arg-40 to Ser-49.
HWLHW89R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1500 as residues: Asn-1 to Lys-16. Glu-32 to Ser-41. Leu-57 to Gly-71.
HWLJL19R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1506 as residues: Arg-46 to Phe-58.
HWLKG82R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1508 as residues: Pro-5 to Gly-25. Ser-29 to Leu-36. Arg-49 to Phe-55.
HWLKM86R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1512 as

	residues: Arg-10 to Lys-23.
HWLQS83R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1515 as residues: Ala-1 to Arg-6.
HWLRP86R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1518 as residues: Tyr-3 to Gly-10.
HWLRQ49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1519 as residues: Pro-19 to Ser-26, Gln-44 to Lys-52.
HWLUF60R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1520 as residues: Gln-7 to Lys-31.
HWLUR41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1522 as residues: Ser-24 to Trp-30.
HWLVD60R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1523 as residues: Cys-15 to Lys-51.
HWMAN61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1525 as residues: Ser-21 to Asp-26.
HWMEH26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1528 as residues: Ser-16 to His-46, Arg-49 to Thr-58.
HWMEL50R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1529 as residues: Pro-24 to Thr-40, Phe-63 to Arg-69.
HWMFB31R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1530 as residues: Asn-2 to Lys-10, Cys-16 to Pro-28, Ser-36 to Glu-41.
HWMFO93R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1532 as residues: Ser-8 to Gln-14.
HMAFE48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1537 as residues: Glu-9 to Gly-17.
HRODJ88R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1538 as residues: Gly-6 to Tyr-14.
HWLAR31R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1539 as residues: Glu-9 to Gly-17.
H2LAU24R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1541 as residues: Glu-11 to Gly-19.
HATDR94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1542 as residues: Glu-14 to Lys-19, Asn-21 to Gly-27.
HWLLI85R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1543 as residues: Val-19 to Asn-32.
HSYCH41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1545 as residues: Thr-71 to Ile-79.

The present invention encompasses polypeptides comprising, or alternatively consisting of, an epitope of the polypeptide sequence shown in SEQ ID NO:Y, or an epitope of the polypeptide sequence encoded by the cDNA in the related cDNA clone contained in a deposited library or encoded by a polynucleotide that hybridizes to the complement of an epitope encoding sequence of SEQ ID NO:X, or an epitope encoding sequence contained in the deposited cDNA clone under stringent hybridization conditions, or alternatively, under lower stringency hybridization conditions, as defined supra. The present invention further encompasses polynucleotide sequences encoding an epitope of a polypeptide sequence of the invention (such as, for example, the sequence disclosed in SEQ ID NO:X), polynucleotide sequences of the complementary strand of a polynucleotide sequence encoding an epitope of the invention, and polynucleotide sequences which hybridize to this complementary strand under stringent hybridization conditions or alternatively, under lower stringency hybridization conditions, as defined supra.

The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably in a human. In a preferred embodiment, the present invention encompasses a polypeptide comprising an epitope, as well as the polynucleotide encoding this polypeptide. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an antibody response in an animal, as determined by any method known in the art, for example, by the methods for generating antibodies described infra. (See, for example, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983)). The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody can immunospecifically bind its antigen as determined by any method well known in the art, for example, by the immunoassays described herein. Immunospecific binding excludes non-specific binding but does not necessarily exclude cross-reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic.

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at

least 50, and, most preferably, between about 15 to about 30 amino acids. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length. Additional non-exclusive preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as portions thereof. Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. Preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these antigenic epitopes. Antigenic epitopes can be used as the target molecules in immunoassays. (See, for instance, Wilson et al., Cell 10 37:767-778 (1984); Sutcliffe et al., Science 219:660-666 (1983)).

Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., *supra*; Wilson et al., *supra*; Chow et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle et al., J. Gen. Virol. 66:2347-2354 (1985). Preferred immunogenic epitopes include the immunogenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these immunogenic epitopes. The polypeptides comprising one or more immunogenic epitopes may be presented for eliciting an antibody response together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse), or, if the polypeptide is of sufficient length (at least about 25 amino acids), the polypeptide may be presented without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting).

Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, *in vivo* immunization, *in vitro* immunization, and phage display methods. See, e.g., Sutcliffe et al., *supra*; Wilson et al., *supra*, and Bittle et al., J. Gen. Virol., 66:2347-2354 (1985). If *in vivo* immunization is used, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine residues may be coupled to a carrier using a linker such as maleimidobenzoyl- N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice

are immunized with either free or carrier- coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg of peptide or carrier protein and Freund's adjuvant or any other adjuvant known for stimulating an immune response. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

As one of skill in the art will appreciate, and as discussed above, the polypeptides of the present invention , and immunogenic and/or antigenic epitope fragments thereof can be fused to other polypeptide sequences. For example, the polypeptides of the present invention may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof) resulting in chimeric polypeptides. Such fusion proteins may facilitate purification and may increase half-life in vivo. This has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. See, e.g., EP 394,827; Traunecker et al., Nature, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT Publications WO 96/22024 and WO 99/04813). IgG Fusion proteins that have a disulfide-linked dimeric structure due to the IgG portion desulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than monomeric polypeptides or fragments thereof alone. See, e.g., Fountoulakis et al., J. Biochem., 270:3958-3964 (1995).

Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, may be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for

immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

5 Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et
10 al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

15 Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

Nucleic acids encoding the above epitopes can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin ("HA") tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed
20 in human cell lines (Janknecht et al., Proc. Natl. Acad. Sci. USA 88:8972- 897 (1991)). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto
25 Ni²⁺ nitriloacetic acid-agarose column and histidine-tagged proteins can be selectively eluted with imidazole-containing buffers.

Additional fusion proteins of the invention may be generated through the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to modulate the activities
30 of polypeptides of the invention, such methods can be used to generate polypeptides with altered activity, as well as agonists and antagonists of the polypeptides. See, generally, U.S. Patent Nos. 5,605,793; 5,811,238; 5,830,721; 5,834,252; and 5,837,458, and Patten et al.,

- Curr. Opinion Biotechnol. 8:724-33 (1997); Harayama, Trends Biotechnol. 16(2):76-82 (1998); Hansson, et al., J. Mol. Biol. 287:265-76 (1999); and Lorenzo and Blasco, Biotechniques 24(2):308- 13 (1998) (each of these patents and publications are hereby incorporated by reference in its entirety). In one embodiment, alteration of polynucleotides corresponding to SEQ ID NO:X and the polypeptides encoded by these polynucleotides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments by homologous or site-specific recombination to generate variation in the polynucleotide sequence. In another embodiment, polynucleotides of the invention, or the encoded polypeptides, may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of a polynucleotide encoding a polypeptide of the invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.
- As discussed herein, any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, polypeptides of the present invention which are shown to be secreted can be used as targeting molecules once fused to other proteins.
- Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.
- In certain preferred embodiments, proteins of the invention comprise fusion proteins wherein the polypeptides are N and/or C-terminal deletion mutants. In preferred embodiments, the application is directed to nucleic acid molecules at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequences encoding polypeptides having the amino acid sequence of the specific N- and C-terminal deletions mutants. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

10 **Vectors, Host Cells, and Protein Production**

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

15 The polynucleotides of the invention may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

20 The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

25 As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include,

but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells (e.g., *Saccharomyces cerevisiae* or *Pichia pastoris* (ATCC Accession No. 201178)); insect cells such as *Drosophila S2* and *Spodoptera Sf9* cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells.

- 5 Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-10 3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Preferred expression vectors for use in yeast systems include, but are not limited to pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalph, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, 15 pPIC3.5K, pPIC9K, and PAO815 (all available from Invitrogen, Carlsbad, CA). Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in 20 many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid 25 extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention can also be recovered from: products purified 30 from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast,

higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

In one embodiment, the yeast *Pichia pastoris* is used to express polypeptides of the invention in a eukaryotic system. *Pichia pastoris* is a methylotrophic yeast which can metabolize methanol as its sole carbon source. A main step in the methanol metabolism pathway is the oxidation of methanol to formaldehyde using O₂. This reaction is catalyzed by the enzyme alcohol oxidase. In order to metabolize methanol as its sole carbon source, *Pichia pastoris* must generate high levels of alcohol oxidase due, in part, to the relatively low affinity of alcohol oxidase for O₂. Consequently, in a growth medium depending on methanol as a main carbon source, the promoter region of one of the two alcohol oxidase genes (*AOX1*) is highly active. In the presence of methanol, alcohol oxidase produced from the *AOX1* gene comprises up to approximately 30% of the total soluble protein in *Pichia pastoris*. See, Ellis, S.B., et al., *Mol. Cell. Biol.* 5:1111-21 (1985); Koutz, P.J., et al., *Yeast* 5:167-77 (1989); Tschopp, J.F., et al., *Nucl. Acids Res.* 15:3859-76 (1987). Thus, a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, under the transcriptional regulation of all or part of the *AOX1* regulatory sequence is expressed at exceptionally high levels in *Pichia* yeast grown in the presence of methanol.

In one example, the plasmid vector pPIC9K is used to express DNA encoding a polypeptide of the invention, as set forth herein, in a *Pichea* yeast system essentially as described in "Pichia Protocols: Methods in Molecular Biology," D.R. Higgins and J. Cregg, eds. The Humana Press, Totowa, NJ, 1998. This expression vector allows expression and secretion of a polypeptide of the invention by virtue of the strong *AOX1* promoter linked to

the *Pichia pastoris* alkaline phosphatase (PHO) secretory signal peptide (i.e., leader) located upstream of a multiple cloning site.

Many other yeast vectors could be used in place of pPIC9K, such as, pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalpha, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, 5 pPIC3.5K, and PAO815, as one skilled in the art would readily appreciate, as long as the proposed expression construct provides appropriately located signals for transcription, translation, secretion (if desired), and the like, including an in-frame AUG as required.

In another embodiment, high-level expression of a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, may be achieved by cloning 10 the heterologous polynucleotide of the invention into an expression vector such as, for example, pGAPZ or pGAPZalpha, and growing the yeast culture in the absence of methanol.

In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or 15 replace endogenous genetic material (e.g., coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with polynucleotides of the invention, and which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous 20 polynucleotide sequences via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their 25 entireties).

In addition, polypeptides of the invention can be chemically synthesized using techniques known in the art (e.g., see Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman & Co., N.Y., and Hunkapiller et al., *Nature*, 310:105-111 (1984)). For example, a polypeptide corresponding to a fragment of a polypeptide can be synthesized 30 by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the

polypeptide sequence. Non-classical amino acids include, but are not limited to, to the D-isomers of the common amino acids, 2,4-diaminobutyric acid, a-amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, g-Abu, e-Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, 5 hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, b-alanine, fluoro-amino acids, designer amino acids such as b-methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

10 Non-naturally occurring variants may be produced using art-known mutagenesis techniques, which include, but are not limited to oligonucleotide mediated mutagenesis, alanine scanning, PCR mutagenesis, site directed mutagenesis (*see, e.g.*, Carter *et al.*, *Nucl. Acids Res.* 13:4331 (1986); and Zoller *et al.*, *Nucl. Acids Res.* 10:6487 (1982)), cassette mutagenesis (*see, e.g.*, Wells *et al.*, *Gene* 34:315 (1985)), restriction selection mutagenesis 15 (*see, e.g.*, Wells *et al.*, *Philos. Trans. R. Soc. London SerA* 317:415 (1986)).

The invention additionally, encompasses polypeptides of the present invention which are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous 20 chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH₄; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

Additional post-translational modifications encompassed by the invention include, for 25 example, e.g., N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of prokaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, 30 isotopic or affinity label to allow for detection and isolation of the protein.

Also provided by the invention are chemically modified derivatives of the polypeptides of the invention which may provide additional advantages such as increased

solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The 5 polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between about 1 kDa and about 10 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the 15 polyethylene glycol to a therapeutic protein or analog). For example, the polyethylene glycol may have an average molecular weight of about 200; 500; 1000; 1500; 2000; 2500; 3000; 3500; 4000; 4500; 5000; 5500; 6000; 6500; 7000; 7500; 8000; 8500; 9000; 9500; 10,000; 10,500; 11,000; 11,500; 12,000; 12,500; 13,000; 13,500; 14,000; 14,500; 15,000; 15,500; 16,000; 16,500; 17,000; 17,500; 18,000; 18,500; 19,000; 19,500; 20,000; 25,000; 30,000; 20 35,000; 40,000; 50,000; 55,000; 60,000; 65,000; 70,000; 75,000; 80,000; 85,000; 90,000; 95,000; or 100,000 kDa.

As noted above, the polyethylene glycol may have a branched structure. Branched polyethylene glycals are described, for example, in U.S. Patent No. 5,643,575; Morpurgo *et al.*, *Appl. Biochem. Biotechnol.* 56:59-72 (1996); Vorobjev *et al.*, *Nucleosides Nucleotides* 25 18:2745-2750 (1999); and Caliceti *et al.*, *Bioconjug. Chem.* 10:638-646 (1999), the disclosures of each of which are incorporated herein by reference.

The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art, e.g., EP 0 401 30 384, herein incorporated by reference (coupling PEG to G-CSF), see also Malik *et al.*, *Exp. Hematol.* 20:1028-1035 (1992) (reporting pegylation of GM-CSF using tresyl chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a

reactive group, such as, a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues; those having a free carboxyl group may include aspartic acid residues glutamic acid residues and 5 the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. Preferred for therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group.

As suggested above, polyethylene glycol may be attached to proteins via linkage to any of a number of amino acid residues. For example, polyethylene glycol can be linked to a 10 proteins via covalent bonds to lysine, histidine, aspartic acid, glutamic acid, or cysteine residues. One or more reaction chemistries may be employed to attach polyethylene glycol to specific amino acid residues (e.g., lysine, histidine, aspartic acid, glutamic acid, or cysteine) of the protein or to more than one type of amino acid residue (e.g., lysine, histidine, aspartic acid, glutamic acid, cysteine and combinations thereof) of the protein.

15 One may specifically desire proteins chemically modified at the N-terminus. Using polyethylene glycol as an illustration of the present composition, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining 20 the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective proteins chemically modified at the N-terminus modification may be accomplished by reductive alkylation which exploits differential 25 reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved.

As indicated above, pegylation of the proteins of the invention may be accomplished 30 by any number of means. For example, polyethylene glycol may be attached to the protein either directly or by an intervening linker. Linkerless systems for attaching polyethylene glycol to proteins are described in Delgado *et al.*, *Crit. Rev. Thera. Drug Carrier Sys.* 9:249-

304 (1992); Francis *et al.*, *Intern. J. of Hematol.* 68:1-18 (1998); U.S. Patent No. 4,002,531; U.S. Patent No. 5,349,052; WO 95/06058; and WO 98/32466, the disclosures of each of which are incorporated herein by reference.

One system for attaching polyethylene glycol directly to amino acid residues of proteins without an intervening linker employs tresylated MPEG, which is produced by the modification of monmethoxy polyethylene glycol (MPEG) using tresylchloride ($\text{ClSO}_2\text{CH}_2\text{CF}_3$). Upon reaction of protein with tresylated MPEG, polyethylene glycol is directly attached to amine groups of the protein. Thus, the invention includes protein-polyethylene glycol conjugates produced by reacting proteins of the invention with a polyethylene glycol molecule having a 2,2,2-trifluoroethane sulphonyl group.

Polyethylene glycol can also be attached to proteins using a number of different intervening linkers. For example, U.S. Patent No. 5,612,460, the entire disclosure of which is incorporated herein by reference, discloses urethane linkers for connecting polyethylene glycol to proteins. Protein-polyethylene glycol conjugates wherein the polyethylene glycol is attached to the protein by a linker can also be produced by reaction of proteins with compounds such as MPEG-succinimidylsuccinate, MPEG activated with 1,1'-carbonyldiimidazole, MPEG-2,4,5-trichloropenylcarbonate, MPEG-p-nitrophenolcarbonate, and various MPEG-succinate derivatives. A number additional polyethylene glycol derivatives and reaction chemistries for attaching polyethylene glycol to proteins are described in WO 98/32466, the entire disclosure of which is incorporated herein by reference. Pegylated protein products produced using the reaction chemistries set out herein are included within the scope of the invention.

The number of polyethylene glycol moieties attached to each protein of the invention (*i.e.*, the degree of substitution) may also vary. For example, the pegylated proteins of the invention may be linked, on average, to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, or more polyethylene glycol molecules. Similarly, the average degree of substitution within ranges such as 1-3, 2-4, 3-5, 4-6, 5-7, 6-8, 7-9, 8-10, 9-11, 10-12, 11-13, 12-14, 13-15, 14-16, 15-17, 16-18, 17-19, or 18-20 polyethylene glycol moieties per protein molecule. Methods for determining the degree of substitution are discussed, for example, in Delgado *et al.*, *Crit. Rev. Therap. Drug Carrier Sys.* 9:249-304 (1992).

The colon cancer antigen polypeptides of the invention may be in monomers or multimers (*i.e.*, dimers, trimers, tetramers and higher multimers). Accordingly, the present

invention relates to monomers and multimers of the polypeptides of the invention, their preparation, and compositions (preferably, Therapeutics) containing them. In specific embodiments, the polypeptides of the invention are monomers, dimers, trimers or tetramers. In additional embodiments, the multimers of the invention are at least dimers, at least trimers, 5 or at least tetramers.

Multimers encompassed by the invention may be homomers or heteromers. As used herein, the term homomer, refers to a multimer containing only polypeptides corresponding to the amino acid sequence of SEQ ID NO:Y or an amino acid sequence encoded by SEQ ID NO:X, and/or an amino acid sequence encoded by the cDNA in a related cDNA clone 10 contained in a deposited library (including fragments, variants, splice variants, and fusion proteins, corresponding to any one of these as described herein). These homomers may contain polypeptides having identical or different amino acid sequences. In a specific embodiment, a homomer of the invention is a multimer containing only polypeptides having an identical amino acid sequence. In another specific embodiment, a homomer of the 15 invention is a multimer containing polypeptides having different amino acid sequences. In specific embodiments, the multimer of the invention is a homodimer (e.g., containing polypeptides having identical or different amino acid sequences) or a homotrimer (e.g., containing polypeptides having identical and/or different amino acid sequences). In additional embodiments, the homomeric multimer of the invention is at least a homodimer, at 20 least a homotrimer, or at least a homotetramer.

As used herein, the term heteromer refers to a multimer containing one or more heterologous polypeptides (i.e., polypeptides of different proteins) in addition to the polypeptides of the invention. In a specific embodiment, the multimer of the invention is a heterodimer, a heterotrimer, or a heterotetramer. In additional embodiments, the heteromeric 25 multimer of the invention is at least a heterodimer, at least a heterotrimer, or at least a heterotetramer.

Multimers of the invention may be the result of hydrophobic, hydrophilic, ionic and/or covalent associations and/or may be indirectly linked, by for example, liposome formation. Thus, in one embodiment, multimers of the invention, such as, for example, 30 homodimers or homotrimers, are formed when polypeptides of the invention contact one another in solution. In another embodiment, heteromultimers of the invention, such as, for example, heterotrimers or heterotetramers, are formed when polypeptides of the invention

contact antibodies to the polypeptides of the invention (including antibodies to the heterologous polypeptide sequence in a fusion protein of the invention) in solution. In other embodiments, multimers of the invention are formed by covalent associations with and/or between the polypeptides of the invention. Such covalent associations may involve one or

5 more amino acid residues contained in the polypeptide sequence (e.g., that recited in SEQ ID NO:Y, or contained in a polypeptide encoded by SEQ ID NO:X, and/or by the cDNA in the related cDNA clone contained in a deposited library). In one instance, the covalent associations are cross-linking between cysteine residues located within the polypeptide sequences which interact in the native (i.e., naturally occurring) polypeptide. In another

10 instance, the covalent associations are the consequence of chemical or recombinant manipulation. Alternatively, such covalent associations may involve one or more amino acid residues contained in the heterologous polypeptide sequence in a fusion protein. In one example, covalent associations are between the heterologous sequence contained in a fusion protein of the invention (see, e.g., US Patent Number 5,478,925). In a specific example, the

15 covalent associations are between the heterologous sequence contained in a Fc fusion protein of the invention (as described herein). In another specific example, covalent associations of fusion proteins of the invention are between heterologous polypeptide sequence from another protein that is capable of forming covalently associated multimers, such as for example, oseteoprotegerin (see, e.g., International Publication NO: WO 98/49305, the contents of

20 which are herein incorporated by reference in its entirety). In another embodiment, two or more polypeptides of the invention are joined through peptide linkers. Examples include those peptide linkers described in U.S. Pat. No. 5,073,627 (hereby incorporated by reference). Proteins comprising multiple polypeptides of the invention separated by peptide linkers may be produced using conventional recombinant DNA technology.

25 Another method for preparing multimer polypeptides of the invention involves use of polypeptides of the invention fused to a leucine zipper or isoleucine zipper polypeptide sequence. Leucine zipper and isoleucine zipper domains are polypeptides that promote multimerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., Science 240:1759, (1988)),

30 and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble multimeric proteins of the

invention are those described in PCT application WO 94/10308, hereby incorporated by reference. Recombinant fusion proteins comprising a polypeptide of the invention fused to a polypeptide sequence that dimerizes or trimerizes in solution are expressed in suitable host cells, and the resulting soluble multimeric fusion protein is recovered from the culture 5 supernatant using techniques known in the art.

Trimeric polypeptides of the invention may offer the advantage of enhanced biological activity. Preferred leucine zipper moieties and isoleucine moieties are those that preferentially form trimers. One example is a leucine zipper derived from lung surfactant protein D (SPD), as described in Hoppe et al. (FEBS Letters 344:191, (1994)) and in U.S. 10 patent application Ser. No. 08/446,922, hereby incorporated by reference. Other peptides derived from naturally occurring trimeric proteins may be employed in preparing trimeric polypeptides of the invention.

In another example, proteins of the invention are associated by interactions between Flag® polypeptide sequence contained in fusion proteins of the invention containing Flag® 15 polypeptide sequence. In a further embodiment, associations proteins of the invention are associated by interactions between heterologous polypeptide sequence contained in Flag® fusion proteins of the invention and anti-Flag® antibody.

The multimers of the invention may be generated using chemical techniques known in the art. For example, polypeptides desired to be contained in the multimers of the invention 20 may be chemically cross-linked using linker molecules and linker molecule length optimization techniques known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Additionally, multimers of the invention may be generated using techniques known in the art to form one or more inter-molecule cross-links between the cysteine residues located within the sequence of the polypeptides 25 desired to be contained in the multimer (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Further, polypeptides of the invention may be routinely modified by the addition of cysteine or biotin to the C-terminus or N-terminus of the polypeptide and techniques known in the art may be applied to generate multimers containing one or more of these modified polypeptides (see, e.g., US Patent Number 30 5,478,925, which is herein incorporated by reference in its entirety). Additionally, techniques known in the art may be applied to generate liposomes containing the polypeptide

components desired to be contained in the multimer of the invention (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

Alternatively, multimers of the invention may be generated using genetic engineering techniques known in the art. In one embodiment, polypeptides contained in multimers of the invention are produced recombinantly using fusion protein technology described herein or otherwise known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In a specific embodiment, polynucleotides coding for a homodimer of the invention are generated by ligating a polynucleotide sequence encoding a polypeptide of the invention to a sequence encoding a linker polypeptide and then further to a synthetic polynucleotide encoding the translated product of the polypeptide in the reverse orientation from the original C-terminus to the N-terminus (lacking the leader sequence) (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In another embodiment, recombinant techniques described herein or otherwise known in the art are applied to generate recombinant polypeptides of the invention which contain a transmembrane domain (or hydrophobic or signal peptide) and which can be incorporated by membrane reconstitution techniques into liposomes (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

Antibodies

Further polypeptides of the invention relate to antibodies and T-cell antigen receptors (TCR) which immunospecifically bind a polypeptide, polypeptide fragment, or variant of SEQ ID NO:Y, and/or an epitope, of the present invention (as determined by immunoassays well known in the art for assaying specific antibody-antigen binding). Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab') fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), and epitope-binding fragments of any of the above. The term "antibody," as used herein, refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that immunospecifically binds an antigen. The immunoglobulin molecules of the invention can be of any type (e.g., IgG,

IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule.

Most preferably the antibodies are human antigen-binding antibody fragments of the present invention and include, but are not limited to, Fab, Fab' and F(ab')2, Fd, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a VL or VH domain. Antigen-binding antibody fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entirety or a portion of the following: hinge region, CH1, CH2, and CH3 domains. Also included in the invention are antigen-binding fragments also comprising any combination of variable region(s) with a hinge region, CH1, CH2, and CH3 domains. The antibodies of the invention may be from any animal origin including birds and mammals. Preferably, the antibodies are human, murine (e.g., mouse and rat), donkey, sheep, rabbit, goat, guinea pig, camel, horse, or chicken. As used herein, "human" antibodies include antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins, as described infra and, for example in, U.S. Patent No. 5,939,598 by Kucherlapati et al.

The antibodies of the present invention may be monospecific, bispecific, trispecific or of greater multispecificity. Multispecific antibodies may be specific for different epitopes of a polypeptide of the present invention or may be specific for both a polypeptide of the present invention as well as for a heterologous epitope, such as a heterologous polypeptide or solid support material. See, e.g., PCT publications WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt, et al., J. Immunol. 147:60-69 (1991); U.S. Patent Nos. 4,474,893; 4,714,681; 4,925,648; 5,573,920; 5,601,819; Kostelny et al., J. Immunol. 148:1547-1553 (1992).

Antibodies of the present invention may be described or specified in terms of the epitope(s) or portion(s) of a polypeptide of the present invention which they recognize or specifically bind. The epitope(s) or polypeptide portion(s) may be specified as described herein, e.g., by N-terminal and C-terminal positions, or by size in contiguous amino acid residues. Antibodies which specifically bind any epitope or polypeptide of the present invention may also be excluded. Therefore, the present invention includes antibodies that

specifically bind polypeptides of the present invention, and allows for the exclusion of the same.

- Antibodies of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies that do not bind any other analog, ortholog, or homolog of
- 5 a polypeptide of the present invention are included. Antibodies that bind polypeptides with at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, and at least 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In specific embodiments, antibodies of the present invention cross-react
- 10 with murine, rat and/or rabbit homologs of human proteins and the corresponding epitopes thereof. Antibodies that do not bind polypeptides with less than 95%, less than 90%, less than 85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, and less than 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention.
- 15 In a specific embodiment, the above-described cross-reactivity is with respect to any single specific antigenic or immunogenic polypeptide, or combination(s) of 2, 3, 4, 5, or more of the specific antigenic and/or immunogenic polypeptides disclosed herein. Further included in the present invention are antibodies which bind polypeptides encoded by polynucleotides which hybridize to a polynucleotide of the present invention under stringent hybridization
- 20 conditions (as described herein). Antibodies of the present invention may also be described or specified in terms of their binding affinity to a polypeptide of the invention. Preferred binding affinities include those with a dissociation constant or Kd less than 5×10^{-2} M, 10^{-2} M, 5×10^{-3} M, 10^{-3} M, 5×10^{-4} M, 10^{-4} M, 5×10^{-5} M, 10^{-5} M, 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7} M, 5×10^{-8} M, 10^{-8} M, 5×10^{-9} M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10^{-15} M, or 10^{-15} M.
- 25

The invention also provides antibodies that competitively inhibit binding of an antibody to an epitope of the invention as determined by any method known in the art for determining competitive binding, for example, the immunoassays described herein. In preferred embodiments, the antibody competitively inhibits binding to the epitope by at least

30 95%, at least 90%, at least 85 %, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50%.

- Antibodies of the present invention may act as agonists or antagonists of the polypeptides of the present invention. For example, the present invention includes antibodies which disrupt the receptor/ligand interactions with the polypeptides of the invention either partially or fully. Preferably, antibodies of the present invention bind an antigenic epitope disclosed herein, or a portion thereof. The invention features both receptor-specific antibodies and ligand-specific antibodies. The invention also features receptor-specific antibodies which do not prevent ligand binding but prevent receptor activation. Receptor activation (i.e., signaling) may be determined by techniques described herein or otherwise known in the art. For example, receptor activation can be determined by detecting the phosphorylation (e.g., tyrosine or serine/threonine) of the receptor or its substrate by immunoprecipitation followed by western blot analysis (for example, as described supra). In specific embodiments, antibodies are provided that inhibit ligand activity or receptor activity by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50% of the activity in absence of the antibody.
- The invention also features receptor-specific antibodies which both prevent ligand binding and receptor activation as well as antibodies that recognize the receptor-ligand complex, and, preferably, do not specifically recognize the unbound receptor or the unbound ligand. Likewise, included in the invention are neutralizing antibodies which bind the ligand and prevent binding of the ligand to the receptor, as well as antibodies which bind the ligand, thereby preventing receptor activation, but do not prevent the ligand from binding the receptor. Further included in the invention are antibodies which activate the receptor. These antibodies may act as receptor agonists, i.e., potentiate or activate either all or a subset of the biological activities of the ligand-mediated receptor activation, for example, by inducing dimerization of the receptor. The antibodies may be specified as agonists, antagonists or inverse agonists for biological activities comprising the specific biological activities of the peptides of the invention disclosed herein. The above antibody agonists can be made using methods known in the art. See, e.g., PCT publication WO 96/40281; U.S. Patent No. 5,811,097; Deng et al., Blood 92(6):1981-1988 (1998); Chen et al., Cancer Res. 58(16):3668-3678 (1998); Harrop et al., J. Immunol. 161(4):1786-1794 (1998); Zhu et al., Cancer Res. 58(15):3209-3214 (1998); Yoon et al., J. Immunol. 160(7):3170-3179 (1998); Prat et al., J. Cell. Sci. 111(Pt2):237-247 (1998); Pitard et al., J. Immunol. Methods 205(2):177-190 (1997); Liautard et al., Cytokine 9(4):233-241 (1997); Carlson et al., J. Biol.

Chem. 272(17):11295-11301 (1997); Taryman et al., Neuron 14(4):755-762 (1995); Muller et al., Structure 6(9):1153-1167 (1998); Bartunek et al., Cytokine 8(1):14-20 (1996) (which are all incorporated by reference herein in their entireties).

Antibodies of the present invention may be used, for example, but not limited to, to purify, detect, and target the polypeptides of the present invention, including both *in vitro* and *in vivo* diagnostic and therapeutic methods. For example, the antibodies have use in immunoassays for qualitatively and quantitatively measuring levels of the polypeptides of the present invention in biological samples. See, e.g., Harlow et al., *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988) (incorporated by reference herein in its entirety).

As discussed in more detail below, the antibodies of the present invention may be used either alone or in combination with other compositions. The antibodies may further be recombinantly fused to a heterologous polypeptide at the N- or C-terminus or chemically conjugated (including covalently and non-covalently conjugations) to polypeptides or other compositions. For example, antibodies of the present invention may be recombinantly fused or conjugated to molecules useful as labels in detection assays and effector molecules such as heterologous polypeptides, drugs, radionuclides, or toxins. See, e.g., PCT publications WO 92/08495; WO 91/14438; WO 89/12624; U.S. Patent No. 5,314,995; and EP 396,387.

The antibodies of the invention include derivatives that are modified, i.e., by the covalent attachment of any type of molecule to the antibody such that covalent attachment does not prevent the antibody from generating an anti-idiotypic response. For example, but not by way of limitation, the antibody derivatives include antibodies that have been modified, e.g., by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Additionally, the derivative may contain one or more non-classical amino acids.

The antibodies of the present invention may be generated by any suitable method known in the art. Polyclonal antibodies to an antigen-of-interest can be produced by various procedures well known in the art. For example, a polypeptide of the invention can be administered to various host animals including, but not limited to, rabbits, mice, rats, etc. to

induce the production of sera containing polyclonal antibodies specific for the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species, and include but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and corynebacterium parvum. Such adjuvants are also well known in the art.

Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technologies, or a combination thereof. For example, monoclonal antibodies can be produced using hybridoma techniques including those known in the art and taught, for example, in Harlow et al., *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: *Monoclonal Antibodies and T-Cell Hybridomas* 563-681 (Elsevier, N.Y., 1981) (said references incorporated by reference in their entireties). The term "monoclonal antibody" as used herein is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art and are discussed in detail in the Examples. In a non-limiting example, mice can be immunized with a polypeptide of the invention or a cell expressing such peptide. Once an immune response is detected, e.g., antibodies specific for the antigen are detected in the mouse serum, the mouse spleen is harvested and splenocytes isolated. The splenocytes are then fused by well known techniques to any suitable myeloma cells, for example cells from cell line SP20 available from the ATCC. Hybridomas are selected and cloned by limited dilution. The hybridoma clones are then assayed by methods known in the art for cells that secrete antibodies capable of binding a polypeptide of the invention. Ascites fluid, which generally contains high levels of antibodies, can be generated by immunizing mice with positive hybridoma clones.

Accordingly, the present invention provides methods of generating monoclonal antibodies as well as antibodies produced by the method comprising culturing a hybridoma cell secreting an antibody of the invention wherein, preferably, the hybridoma is generated by

fusing splenocytes isolated from a mouse immunized with an antigen of the invention with myeloma cells and then screening the hybridomas resulting from the fusion for hybridoma clones that secrete an antibody able to bind a polypeptide of the invention.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, Fab and F(ab')2 fragments of the invention may be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). F(ab')2 fragments contain the variable region, the light chain constant region and the CH1 domain of the heavy chain.

For example, the antibodies of the present invention can also be generated using various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In a particular embodiment, such phage can be utilized to display antigen binding domains expressed from a repertoire or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds the antigen of interest can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13 binding domains expressed from phage with Fab, Fv or disulfide stabilized Fv antibody domains recombinantly fused to either the phage gene III or gene VIII protein. Examples of phage display methods that can be used to make the antibodies of the present invention include those disclosed in Brinkman et al., J. Immunol. Methods 182:41-50 (1995); Ames et al., J. Immunol. Methods 184:177-186 (1995); Kettleborough et al., Eur. J. Immunol. 24:952-958 (1994); Persic et al., Gene 187 9-18 (1997); Burton et al., Advances in Immunology 57:191-280 (1994); PCT application No. PCT/GB91/01134; PCT publications WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Patent Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as

described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab')2 fragments can also be employed using methods known in the art such as those disclosed in PCT publication WO 92/22324; Mullinax et al., BioTechniques 12(6):864-869 (1992); and Sawai et al., AJRI 34:26-34 (1995); and Better et al., Science 240:1041-1043 5 (1988) (said references incorporated by reference in their entireties).

Examples of techniques which can be used to produce single-chain Fvs and antibodies include those described in U.S. Patents 4,946,778 and 5,258,498; Huston et al., Methods in Enzymology 203:46-88 (1991); Shu et al., PNAS 90:7995-7999 (1993); and Skerra et al., Science 240:1038-1040 (1988). For some uses, including in vivo use of antibodies in 10 humans and in vitro detection assays, it may be preferable to use chimeric, humanized, or human antibodies. A chimeric antibody is a molecule in which different portions of the antibody are derived from different animal species, such as antibodies having a variable region derived from a murine monoclonal antibody and a human immunoglobulin constant region. Methods for producing chimeric antibodies are known in the art. See e.g., Morrison, 15 Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Gillies et al., (1989) J. Immunol. Methods 125:191-202; U.S. Patent Nos. 5,807,715; 4,816,567; and 4,816397, which are incorporated herein by reference in their entirety. Humanized antibodies are 20 antibody molecules from non-human species antibody that binds the desired antigen having one or more complementarity determining regions (CDRs) from the non-human species and a framework regions from a human immunoglobulin molecule. Often, framework residues in the human framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, preferably improve, antigen binding. These framework substitutions are identified by methods well known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important 25 for antigen binding and sequence comparison to identify unusual framework residues at particular positions. (See, e.g., Queen et al., U.S. Patent No. 5,585,089; Riechmann et al., Nature 332:323 (1988), which are incorporated herein by reference in their entireties.) Antibodies can be humanized using a variety of techniques known in the art including, for example, CDR-grafting (EP 239,400; PCT publication WO 91/09967; U.S. Patent Nos. 30 5,225,539; 5,530,101; and 5,585,089), veneering or resurfacing (EP 592,106; EP 519,596; Padlan, Molecular Immunology 28(4/5):489-498 (1991); Studnicka et al., Protein

Engineering 7(6):805-814 (1994); Roguska. et al., PNAS 91:969-973 (1994)), and chain shuffling (U.S. Patent No. 5,565,332).

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Human antibodies can be made by a variety of methods known in the art including phage display methods described above using antibody libraries derived from human immunoglobulin sequences. See also, U.S. Patent Nos. 4,444,887 and 4,716,111; and PCT publications WO 98/46645, WO 98/50433, WO 98/24893, WO 98/16654, WO 96/34096, WO 96/33735, and WO 91/10741; each of which is incorporated herein by reference in its entirety.

Human antibodies can also be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes. For example, the human heavy and light chain immunoglobulin gene complexes may be introduced randomly or by homologous recombination into mouse embryonic stem cells. Alternatively, the human variable region, constant region, and diversity region may be introduced into mouse embryonic stem cells in addition to the human heavy and light chain genes. The mouse heavy and light chain immunoglobulin genes may be rendered non-functional separately or simultaneously with the introduction of human immunoglobulin loci by homologous recombination. In particular, homozygous deletion of the JH region prevents endogenous antibody production. The modified embryonic stem cells are expanded and microinjected into blastocysts to produce chimeric mice. The chimeric mice are then bred to produce homozygous offspring which express human antibodies. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained from the immunized, transgenic mice using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA, IgM and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar, Int. Rev. Immunol. 13:65-93 (1995). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; European Patent

No. 0 598 877; U.S. Patent Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825; 5,661,016; 5,545,806; 5,814,318; 5,885,793; 5,916,771; and 5,939,598, which are incorporated by reference herein in their entirety. In addition, companies such as Abgenix, Inc. (Freemont, CA) and Genpharm (San Jose, CA) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., Bio/technology 12:899-903 (1988)).

Further, antibodies to the polypeptides of the invention can, in turn, be utilized to generate anti-idiotype antibodies that "mimic" polypeptides of the invention using techniques well known to those skilled in the art. (See, e.g., Greenspan & Bona, FASEB J. 7(5):437-444; (1989) and Nissinoff, J. Immunol. 147(8):2429-2438 (1991)). For example, antibodies which bind to and competitively inhibit polypeptide multimerization and/or binding of a polypeptide of the invention to a ligand can be used to generate anti-idiotypes that "mimic" the polypeptide multimerization and/or binding domain and, as a consequence, bind to and neutralize polypeptide and/or its ligand. Such neutralizing anti-idiotypes or Fab fragments of such anti-idiotypes can be used in therapeutic regimens to neutralize polypeptide ligand. For example, such anti-idiotypic antibodies can be used to bind a polypeptide of the invention and/or to bind its ligands/receptors, and thereby block its biological activity.

Polynucleotides Encoding Antibodies

The invention further provides polynucleotides comprising a nucleotide sequence encoding an antibody of the invention and fragments thereof. The invention also encompasses polynucleotides that hybridize under stringent or alternatively, under lower stringency hybridization conditions, e.g., as defined supra, to polynucleotides that encode an antibody, preferably, that specifically binds to a polypeptide of the invention, preferably, an antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO:Y.

The polynucleotides may be obtained, and the nucleotide sequence of the polynucleotides determined, by any method known in the art. For example, if the nucleotide sequence of the antibody is known, a polynucleotide encoding the antibody may be

assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al., BioTechniques 17:242 (1994)), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding the antibody, annealing and ligating of those oligonucleotides, and then amplification of the ligated oligonucleotides by 5 PCR.

Alternatively, a polynucleotide encoding an antibody may be generated from nucleic acid from a suitable source. If a clone containing a nucleic acid encoding a particular antibody is not available, but the sequence of the antibody molecule is known, a nucleic acid encoding the immunoglobulin may be chemically synthesized or obtained from a suitable 10 source (e.g., an antibody cDNA library, or a cDNA library generated from, or nucleic acid, preferably poly A+ RNA, isolated from, any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody of the invention) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence to identify, e.g., a cDNA 15 clone from a cDNA library that encodes the antibody. Amplified nucleic acids generated by PCR may then be cloned into replicable cloning vectors using any method well known in the art.

Once the nucleotide sequence and corresponding amino acid sequence of the antibody is determined, the nucleotide sequence of the antibody may be manipulated using methods 20 well known in the art for the manipulation of nucleotide sequences, e.g., recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., 1990, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY and Ausubel et al., eds., 1998, Current Protocols in Molecular Biology, John Wiley & Sons, NY, which are both incorporated by reference 25 herein in their entireties), to generate antibodies having a different amino acid sequence, for example to create amino acid substitutions, deletions, and/or insertions.

In a specific embodiment, the amino acid sequence of the heavy and/or light chain variable domains may be inspected to identify the sequences of the complementarity determining regions (CDRs) by methods that are well known in the art, e.g., by comparison to 30 known amino acid sequences of other heavy and light chain variable regions to determine the regions of sequence hypervariability. Using routine recombinant DNA techniques, one or more of the CDRs may be inserted within framework regions, e.g., into human framework

regions to humanize a non-human antibody, as described supra. The framework regions may be naturally occurring or consensus framework regions, and preferably human framework regions (see, e.g., Chothia et al., J. Mol. Biol. 278: 457-479 (1998) for a listing of human framework regions). Preferably, the polynucleotide generated by the combination of the framework regions and CDRs encodes an antibody that specifically binds a polypeptide of the invention. Preferably, as discussed supra, one or more amino acid substitutions may be made within the framework regions, and, preferably, the amino acid substitutions improve binding of the antibody to its antigen. Additionally, such methods may be used to make amino acid substitutions or deletions of one or more variable region cysteine residues participating in an intrachain disulfide bond to generate antibody molecules lacking one or more intrachain disulfide bonds. Other alterations to the polynucleotide are encompassed by the present invention and within the skill of the art.

In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., Proc. Natl. Acad. Sci. 81:851-855 (1984); Neuberger et al., Nature 312:604-608 (1984); Takeda et al., Nature 314:452-454 (1985)) by splicing genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. As described supra, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region, e.g., humanized antibodies.

Alternatively, techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778; Bird, Science 242:423- 42 (1988); Huston et al., Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988); and Ward et al., Nature 334:544-54 (1989)) can be adapted to produce single chain antibodies. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide. Techniques for the assembly of functional Fv fragments in E. coli may also be used (Skerra et al., Science 242:1038- 1041 (1988)).

Methods of Producing Antibodies

The antibodies of the invention can be produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis or preferably, by recombinant expression techniques.

- Recombinant expression of an antibody of the invention, or fragment, derivative or analog thereof, (e.g., a heavy or light chain of an antibody of the invention or a single chain antibody of the invention), requires construction of an expression vector containing a polynucleotide that encodes the antibody. Once a polynucleotide encoding an antibody molecule or a heavy or light chain of an antibody, or portion thereof (preferably containing the heavy or light chain variable domain), of the invention has been obtained, the vector for the production of the antibody molecule may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing a protein by expressing a polynucleotide containing an antibody encoding nucleotide sequence are described herein.
- 5 Methods which are well known to those skilled in the art can be used to construct expression vectors containing antibody coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. The invention, thus, provides replicable vectors comprising a nucleotide sequence encoding an antibody molecule
- 10 of the invention, or a heavy or light chain thereof, or a heavy or light chain variable domain, operably linked to a promoter. Such vectors may include the nucleotide sequence encoding the constant region of the antibody molecule (see, e.g., PCT Publication WO 86/05807; PCT Publication WO 89/01036; and U.S. Patent No. 5,122,464) and the variable domain of the antibody may be cloned into such a vector for expression of the entire heavy or light chain.
- 15 The expression vector is transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce an antibody of the invention. Thus, the invention includes host cells containing a polynucleotide encoding an antibody of the invention, or a heavy or light chain thereof, or a single chain antibody of the invention, operably linked to a heterologous promoter. In preferred embodiments for the expression of double-chained antibodies, vectors encoding both the heavy and light chains
- 20 may be co-expressed in the host cell for expression of the entire immunoglobulin molecule, as detailed below.

A variety of host-expression vector systems may be utilized to express the antibody molecules of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding sequences, express an antibody molecule of the invention in situ. These include but are not

limited to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing antibody coding sequences; yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing antibody coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing antibody coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter). Preferably, bacterial cells such as *Escherichia coli*, and more preferably, eukaryotic cells, especially for the expression of whole recombinant antibody molecule, are used for the expression of a recombinant antibody molecule. For example, mammalian cells such as Chinese hamster ovary cells (CHO), in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus is an effective expression system for antibodies (Foecking et al., Gene 45:101 (1986); Cockett et al., Bio/Technology 8:2 (1990)).

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the antibody molecule being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of pharmaceutical compositions of an antibody molecule, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., EMBO J. 2:1791 (1983)), in which the antibody coding sequence may be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, Nucleic Acids Res. 13:3101-3109 (1985); Van Heeke & Schuster, J. Biol. Chem. 24:5503-5509 (1989)); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to matrix glutathione-agarose beads followed by elution in the presence of free

glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells.

- 5 The antibody coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter).

In mammalian host cells, a number of viral-based expression systems may be utilized.

- 10 In cases where an adenovirus is used as an expression vector, the antibody coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by in vitro or in vivo recombination. Insertion in a non- essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing the antibody molecule in infected hosts. (e.g., see Logan & Shenk,
15 Proc. Natl. Acad. Sci. USA 81:355-359 (1984)). Specific initiation signals may also be required for efficient translation of inserted antibody coding sequences. These signals include the ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can
20 be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner et al., Methods in Enzymol. 153:51-544 (1987)).

- 25 In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end,
30 eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERY, BHK, Hela, COS,

MDCK, 293, 3T3, WI38, and in particular, breast cancer cell lines such as, for example, BT483, Hs578T, HTB2, BT20 and T47D, and normal mammary gland cell line such as, for example, CRL7030 and Hs578Bst.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the antibody molecule may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, 10 engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the antibody 15 molecule. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that interact directly or indirectly with the antibody molecule.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler et al., Cell 11:223 (1977)), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, Proc. Natl. Acad. Sci. USA 48:202 20 (1992)), and adenine phosphoribosyltransferase (Lowy et al., Cell 22:817 (1980)) genes can be employed in tk-, hprt- or aprt- cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al., Natl. Acad. Sci. USA 77:357 (1980); O'Hare et al., Proc. Natl. Acad. Sci. USA 78:1527 (1981)); gpt, which confers resistance to mycophenolic acid 25 (Mulligan & Berg, Proc. Natl. Acad. Sci. USA 78:2072 (1981)); neo, which confers resistance to the aminoglycoside G-418 Clinical Pharmacy 12:488-505; Wu and Wu, Biotherapy 3:87-95 (1991); Tolstoshev, Ann. Rev. Pharmacol. Toxicol. 32:573-596 (1993); Mulligan, Science 260:926-932 (1993); and Morgan and Anderson, Ann. Rev. Biochem. 62:191-217 (1993); May, 1993, TIB TECH 11(5):155-215); and hygro, which confers 30 resistance to hygromycin (Santerre et al., Gene 30:147 (1984)). Methods commonly known in the art of recombinant DNA technology may be routinely applied to select the desired recombinant clone, and such methods are described, for example, in Ausubel et al. (eds.),

Current Protocols in Molecular Biology, John Wiley & Sons, NY (1993); Kriegler, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY (1990); and in Chapters 12 and 13, Dracopoli et al. (eds), Current Protocols in Human Genetics, John Wiley & Sons, NY (1994); Colberre-Garapin et al., J. Mol. Biol. 150:1 (1981), which are incorporated by reference herein in their entireties.

The expression levels of an antibody molecule can be increased by vector amplification (for a review, see Bebbington and Hentschel, The use of vectors based on gene amplification for the expression of cloned genes in mammalian cells in DNA cloning, Vol.3. (Academic Press, New York, 1987)). When a marker in the vector system expressing antibody is amplifiable, increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the antibody gene, production of the antibody will also increase (Crouse et al., Mol. Cell. Biol. 3:257 (1983)).

The host cell may be co-transfected with two expression vectors of the invention, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may contain identical selectable markers which enable equal expression of heavy and light chain polypeptides. Alternatively, a single vector may be used which encodes, and is capable of expressing, both heavy and light chain polypeptides. In such situations, the light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, Nature 322:52 (1986); Kohler, Proc. Natl. Acad. Sci. USA 77:2197 (1980)). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA.

Once an antibody molecule of the invention has been produced by an animal, chemically synthesized, or recombinantly expressed, it may be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for the specific antigen after Protein A, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. In addition, the antibodies of the present invention or fragments thereof can be fused to heterologous polypeptide sequences described herein or otherwise known in the art, to facilitate purification.

The present invention encompasses antibodies recombinantly fused or chemically conjugated (including both covalently and non-covalently conjugations) to a polypeptide (or

portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention to generate fusion proteins. The fusion does not necessarily need to be direct, but may occur through linker sequences. The antibodies may be specific for antigens other than polypeptides (or portion thereof, preferably at least 10, 20,
5 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention. For example, antibodies may be used to target the polypeptides of the present invention to particular cell types, either in vitro or in vivo, by fusing or conjugating the polypeptides of the present invention to antibodies specific for particular cell surface receptors. Antibodies fused or conjugated to the polypeptides of the present invention may also be used in in vitro
10 immunoassays and purification methods using methods known in the art. See e.g., Harbor et al., *supra*, and PCT publication WO 93/21232; EP 439,095; Naramura et al., *Immunol. Lett.* 39:91-99 (1994); U.S. Patent 5,474,981; Gillies et al., *PNAS* 89:1428-1432 (1992); Fell et al., *J. Immunol.* 146:2446-2452(1991), which are incorporated by reference in their entireties.

The present invention further includes compositions comprising the polypeptides of the present invention fused or conjugated to antibody domains other than the variable regions.
15 For example, the polypeptides of the present invention may be fused or conjugated to an antibody Fc region, or portion thereof. The antibody portion fused to a polypeptide of the present invention may comprise the constant region, hinge region, CH1 domain, CH2 domain, and CH3 domain or any combination of whole domains or portions thereof. The polypeptides may also be fused or conjugated to the above antibody portions to form multimers. For example, Fc portions fused to the polypeptides of the present invention can form dimers through disulfide bonding between the Fc portions. Higher multimeric forms can be made by fusing the polypeptides to portions of IgA and IgM. Methods for fusing or conjugating the polypeptides of the present invention to antibody portions are known in the
20 art. See, e.g., U.S. Patent Nos. 5,336,603; 5,622,929; 5,359,046; 5,349,053; 5,447,851; 5,112,946; EP 307,434; EP 367,166; PCT publications WO 96/04388; WO 91/06570; Ashkenazi et al., *Proc. Natl. Acad. Sci. USA* 88:10535-10539 (1991); Zheng et al., *J. Immunol.* 154:5590-5600 (1995); and Vil et al., *Proc. Natl. Acad. Sci. USA* 89:11337-11341(1992) (said references incorporated by reference in their entireties).

30 As discussed, supra, the polypeptides corresponding to a polypeptide, polypeptide fragment, or a variant of SEQ ID NO:Y may be fused or conjugated to the above antibody portions to increase the in vivo half life of the polypeptides or for use in immunoassays using

methods known in the art. Further, the polypeptides corresponding to SEQ ID NO:Y may be fused or conjugated to the above antibody portions to facilitate purification. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of 5 mammalian immunoglobulins. (EP 394,827; Traunecker et al., Nature 331:84-86 (1988).

The polypeptides of the present invention fused or conjugated to an antibody having disulfide-linked dimeric structures (due to the IgG) may also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995)). In many cases, the Fc part 10 in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP A 232,262). Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, 15 have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, Bennett et al., J. Molecular Recognition 8:52-58 (1995); Johanson et al., J. Biol. Chem. 270:9459-9471 (1995)).

Moreover, the antibodies or fragments thereof of the present invention can be fused to marker sequences, such as a peptide to facilitate purification. In preferred embodiments, the 20 marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Other peptide tags useful for purification include, but are not limited to, the 25 "HA" tag, which corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson et al., Cell 37:767 (1984)) and the "flag" tag.

The present invention further encompasses antibodies or fragments thereof conjugated to a diagnostic or therapeutic agent. The antibodies can be used diagnostically to, for example, monitor the development or progression of a tumor as part of a clinical testing 30 procedure to, e.g., determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent

materials, bioluminescent materials, radioactive materials, positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions. The detectable substance may be coupled or conjugated either directly to the antibody (or fragment thereof) or indirectly, through an intermediate (such as, for example, a linker known in the art) using techniques known in the art. See, for example, U.S. Patent No. 4,741,900 for metal ions which can be conjugated to antibodies for use as diagnostics according to the present invention. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include 125I, 131I, 111In or 99Tc.

Further, an antibody or fragment thereof may be conjugated to a therapeutic moiety such as a cytotoxin, e.g., a cytostatic or cytoidal agent, a therapeutic agent or a radioactive metal ion, e.g., alpha-emitters such as, for example, 213Bi. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include paclitaxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine).

The conjugates of the invention can be used for modifying a given biological response, the therapeutic agent or drug moiety is not to be construed as limited to classical

chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, α -interferon, β -interferon, nerve growth factor, platelet derived growth factor, 5 tissue plasminogen activator, an apoptotic agent, e.g., TNF-alpha, TNF-beta, AIM I (See, International Publication No. WO 97/33899), AIM II (See, International Publication No. WO 97/34911), Fas Ligand (Takahashi *et al.*, *Int. Immunol.*, 6:1567-1574 (1994)), VEGI (See, International Publication No. WO 99/23105), a thrombotic agent or an anti-angiogenic agent, e.g., angiostatin or endostatin; or, biological response modifiers such as, for example, 10 lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Antibodies may also be attached to solid supports, which are particularly useful for immunoassays or purification of the target antigen. Such solid supports include, but are not 15 limited to, glass, cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, e.g., Armon *et al.*, "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld *et al.* (eds.), pp. 243-56 20 (Alan R. Liss, Inc. 1985); Hellstrom *et al.*, "Antibodies For Drug Delivery", in Controlled Drug Delivery (2nd Ed.), Robinson *et al.* (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in Monoclonal Antibodies '84: Biological And Clinical Applications, Pinchera *et al.* (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of 25 Radiolabeled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin *et al.* (eds.), pp. 303-16 (Academic Press 1985), and Thorpe *et al.*, "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.* 62:119-58 (1982).

Alternatively, an antibody can be conjugated to a second antibody to form an antibody 30 heteroconjugate as described by Segal in U.S. Patent No. 4,676,980, which is incorporated herein by reference in its entirety.

An antibody, with or without a therapeutic moiety conjugated to it, administered alone or in combination with cytotoxic factor(s) and/or cytokine(s) can be used as a therapeutic.

Immunophenotyping

- 5 The antibodies of the invention may be utilized for immunophenotyping of cell lines and biological samples. The translation product of the gene of the present invention may be useful as a cell specific marker, or more specifically as a cellular marker that is differentially expressed at various stages of differentiation and/or maturation of particular cell types. Monoclonal antibodies directed against a specific epitope, or combination of epitopes, will
10 allow for the screening of cellular populations expressing the marker. Various techniques can be utilized using monoclonal antibodies to screen for cellular populations expressing the marker(s), and include magnetic separation using antibody-coated magnetic beads, "panning" with antibody attached to a solid matrix (i.e., plate), and flow cytometry (See, e.g., U.S. Patent 5,985,660; and Morrison *et al.*, *Cell*, 96:737-49 (1999)).
15 These techniques allow for the screening of particular populations of cells, such as might be found with hematological malignancies (i.e. minimal residual disease (MRD) in acute leukemic patients) and "non-self" cells in transplantations to prevent Graft-versus-Host Disease (GVHD). Alternatively, these techniques allow for the screening of hematopoietic stem and progenitor cells capable of undergoing proliferation and/or differentiation, as might
20 be found in human umbilical cord blood.

Assays For Antibody Binding

- The antibodies of the invention may be assayed for immunospecific binding by any method known in the art. The immunoassays which can be used include but are not limited
25 to competitive and non-competitive assay systems using techniques such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name
30 but a few. Such assays are routine and well known in the art (see, e.g., Ausubel et al, eds. 1994, *Current Protocols in Molecular Biology*, Vol. 1, John Wiley & Sons, Inc., New York,

which is incorporated by reference herein in its entirety). Exemplary immunoassays are described briefly below (but are not intended by way of limitation).

Immunoprecipitation protocols generally comprise lysing a population of cells in a lysis buffer such as RIPA buffer (1% NP-40 or Triton X- 100, 1% sodium deoxycholate, 5 0.1% SDS, 0.15 M NaCl, 0.01 M sodium phosphate at pH 7.2, 1% Trasylol) supplemented with protein phosphatase and/or protease inhibitors (e.g., EDTA, PMSF, aprotinin, sodium vanadate), adding the antibody of interest to the cell lysate, incubating for a period of time (e.g., 1-4 hours) at 4° C. adding protein A and/or protein G sepharose beads to the cell lysate, incubating for about an hour or more at 4° C, washing the beads in lysis buffer and 10 resuspending the beads in SDS/sample buffer. The ability of the antibody of interest to immunoprecipitate a particular antigen can be assessed by, e.g., western blot analysis. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the binding of the antibody to an antigen and decrease the background (e.g., pre-clearing the cell lysate with sepharose beads). For further discussion regarding 15 immunoprecipitation protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.16.1.

Western blot analysis generally comprises preparing protein samples, electrophoresis of the protein samples in a polyacrylamide gel (e.g., 8%- 20% SDS-PAGE depending on the molecular weight of the antigen), transferring the protein sample from the polyacrylamide gel 20 to a membrane such as nitrocellulose, PVDF or nylon, blocking the membrane in blocking solution (e.g., PBS with 3% BSA or non-fat milk), washing the membrane in washing buffer (e.g., PBS-Tween 20), blocking the membrane with primary antibody (the antibody of interest) diluted in blocking buffer, washing the membrane in washing buffer, blocking the membrane with a secondary antibody (which recognizes the primary antibody, e.g., an anti- 25 human antibody) conjugated to an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) or radioactive molecule (e.g., ³²P or ¹²⁵I) diluted in blocking buffer, washing the membrane in wash buffer, and detecting the presence of the antigen. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected and to reduce the background noise. For further discussion regarding western 30 blot protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.8.1.

ELISAs comprise preparing antigen, coating the well of a 96 well microtiter plate with the antigen, adding the antibody of interest conjugated to a detectable compound such as an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) to the well and incubating for a period of time, and detecting the presence of the antigen. In ELISAs the antibody of interest does not have to be conjugated to a detectable compound; instead, a second antibody (which recognizes the antibody of interest) conjugated to a detectable compound may be added to the well. Further, instead of coating the well with the antigen, the antibody may be coated to the well. In this case, a second antibody conjugated to a detectable compound may be added following the addition of the antigen of interest to the coated well. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected as well as other variations of ELISAs known in the art. For further discussion regarding ELISAs see, e.g., Ausubel et al, eds. 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 11.2.1.

The binding affinity of an antibody to an antigen and the off-rate of an antibody-antigen interaction can be determined by competitive binding assays. One example of a competitive binding assay is a radioimmunoassay comprising the incubation of labeled antigen (e.g., ³H or ¹²⁵I) with the antibody of interest in the presence of increasing amounts of unlabeled antigen, and the detection of the antibody bound to the labeled antigen. The affinity of the antibody of interest for a particular antigen and the binding off-rates can be determined from the data by scatchard plot analysis. Competition with a second antibody can also be determined using radioimmunoassays. In this case, the antigen is incubated with antibody of interest conjugated to a labeled compound (e.g., ³H or ¹²⁵I) in the presence of increasing amounts of an unlabeled second antibody.

25 *Therapeutic Uses*

The present invention is further directed to antibody-based therapies which involve administering antibodies of the invention to an animal, preferably a mammal, and most preferably a human, patient for treating one or more of the disclosed diseases, disorders, or conditions. Therapeutic compounds of the invention include, but are not limited to, antibodies of the invention (including fragments, analogs and derivatives thereof as described herein) and nucleic acids encoding antibodies of the invention (including fragments, analogs and derivatives thereof and anti-idiotypic antibodies as described herein). The antibodies of

the invention can be used to treat, inhibit or prevent diseases, disorders or conditions associated with aberrant expression and/or activity of a polypeptide of the invention, including, but not limited to, any one or more of the diseases, disorders, or conditions described herein. The treatment and/or prevention of diseases, disorders, or conditions associated with aberrant expression and/or activity of a polypeptide of the invention includes, but is not limited to, alleviating symptoms associated with those diseases, disorders or conditions. Antibodies of the invention may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present invention locally or systemically in the body or by direct cytotoxicity of the antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the art will know how to use the antibodies of the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth factors (such as, e.g., IL-2, IL-3 and IL-7), for example, which serve to increase the number or activity of effector cells which interact with the antibodies.

The antibodies of the invention may be administered alone or in combination with other types of treatments (e.g., radiation therapy, chemotherapy, hormonal therapy, immunotherapy and anti-tumor agents). Generally, administration of products of a species origin or species reactivity (in the case of antibodies) that is the same species as that of the patient is preferred. Thus, in a preferred embodiment, human antibodies, fragments derivatives, analogs, or nucleic acids, are administered to a human patient for therapy or prophylaxis.

It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and therapy of disorders related to polynucleotides or polypeptides, including fragments thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for polynucleotides or polypeptides of the invention, including fragments thereof. Preferred binding affinities

include those with a dissociation constant or Kd less than 5×10^{-2} M, 10^2 M, 5×10^{-3} M, 10^{-3} M, 5×10^{-4} M, 10^{-4} M, 5×10^{-5} M, 10^{-5} M, 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7} M, 5×10^{-8} M, 10^{-8} M, 5×10^{-9} M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10^{-15} M, and 10^{-15} M.

5

Gene Therapy

In a specific embodiment, nucleic acids comprising sequences encoding antibodies or functional derivatives thereof, are administered to treat, inhibit or prevent a disease or disorder associated with aberrant expression and/or activity of a polypeptide of the invention, 10 by way of gene therapy. Gene therapy refers to therapy performed by the administration to a subject of an expressed or expressible nucleic acid. In this embodiment of the invention, the nucleic acids produce their encoded protein that mediates a therapeutic effect.

Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

15 For general reviews of the methods of gene therapy, see Goldspiel et al., Clinical Pharmacy 12:488-505 (1993); Wu and Wu, Biotherapy 3:87-95 (1991); Tolstoshev, Ann. Rev. Pharmacol. Toxicol. 32:573-596 (1993); Mulligan, Science 260:926-932 (1993); and Morgan and Anderson, Ann. Rev. Biochem. 62:191-217 (1993); May, TIBTECH 11(5):155-215 (1993). Methods commonly known in the art of recombinant DNA technology which can 20 be used are described in Ausubel et al. (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, NY (1993); and Kriegler, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY (1990).

25 In a preferred aspect, the compound comprises nucleic acid sequences encoding an antibody, said nucleic acid sequences being part of expression vectors that express the antibody or fragments or chimeric proteins or heavy or light chains thereof in a suitable host. In particular, such nucleic acid sequences have promoters operably linked to the antibody coding region, said promoter being inducible or constitutive, and, optionally, tissue-specific. In another particular embodiment, nucleic acid molecules are used in which the antibody coding sequences and any other desired sequences are flanked by regions that promote 30 homologous recombination at a desired site in the genome, thus providing for intrachromosomal expression of the antibody encoding nucleic acids (Koller and Smithies, Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); Zijlstra et al., Nature 342:435-438 (1989)).

In specific embodiments, the expressed antibody molecule is a single chain antibody; alternatively, the nucleic acid sequences include sequences encoding both the heavy and light chains, or fragments thereof, of the antibody.

Delivery of the nucleic acids into a patient may be either direct, in which case the 5 patient is directly exposed to the nucleic acid or nucleic acid- carrying vectors, or indirect, in which case, cells are first transformed with the nucleic acids in vitro, then transplanted into the patient. These two approaches are known, respectively, as *in vivo* or *ex vivo* gene therapy.

In a specific embodiment, the nucleic acid sequences are directly administered *in vivo*, where it is expressed to produce the encoded product. This can be accomplished by 10 any of numerous methods known in the art, e.g., by constructing them as part of an appropriate nucleic acid expression vector and administering it so that they become intracellular, e.g., by infection using defective or attenuated retrovirals or other viral vectors (see U.S. Patent No. 4,980,286), or by direct injection of naked DNA, or by use of 15 microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, encapsulation in liposomes, microparticles, or microcapsules, or by administering them in linkage to a peptide which is known to enter the nucleus, by administering it in linkage to a ligand subject to receptor-mediated endocytosis (see, e.g., Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987)) (which can be used to target 20 cell types specifically expressing the receptors), etc. In another embodiment, nucleic acid-ligand complexes can be formed in which the ligand comprises a fusogenic viral peptide to disrupt endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted *in vivo* for cell specific uptake and expression, by targeting a specific receptor (see, e.g., PCT Publications WO 92/06180; WO 92/22635; 25 WO92/20316; WO93/14188, WO 93/20221). Alternatively, the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); Zijlstra et al., Nature 342:435-438 (1989)).

In a specific embodiment, viral vectors that contains nucleic acid sequences encoding 30 an antibody of the invention are used. For example, a retroviral vector can be used (see Miller et al., Meth. Enzymol. 217:581-599 (1993)). These retroviral vectors contain the components necessary for the correct packaging of the viral genome and integration into the

host cell DNA. The nucleic acid sequences encoding the antibody to be used in gene therapy are cloned into one or more vectors, which facilitates delivery of the gene into a patient. More detail about retroviral vectors can be found in Boesen et al., Biotherapy 6:291-302 (1994), which describes the use of a retroviral vector to deliver the mdrl gene to 5 hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are: Clowes et al., J. Clin. Invest. 93:644-651 (1994); Kiem et al., Blood 83:1467-1473 (1994); Salmons and Gunzberg, Human Gene Therapy 4:129-141 (1993); and Grossman and Wilson, Curr. Opin. in Genetics and Devel. 3:110-114 (1993).

10 Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are liver, the central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing 15 cells. Kozarsky and Wilson, Current Opinion in Genetics and Development 3:499-503 (1993) present a review of adenovirus-based gene therapy. Bout et al., Human Gene Therapy 5:3-10 (1994) demonstrated the use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., Science 252:431-434 (1991); Rosenfeld et al., Cell 20 68:143- 155 (1992); Mastrangeli et al., J. Clin. Invest. 91:225-234 (1993); PCT Publication WO94/12649; and Wang, et al., Gene Therapy 2:775-783 (1995). In a preferred embodiment, adenovirus vectors are used.

Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., Proc. Soc. Exp. Biol. Med. 204:289-300 (1993); U.S. Patent No. 5,436,146).

25 Another approach to gene therapy involves transferring a gene to cells in tissue culture by such methods as electroporation, lipofection, calcium phosphate mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection to isolate those cells that have taken up and are expressing the transferred gene. Those cells are then delivered to a 30 patient.

In this embodiment, the nucleic acid is introduced into a cell prior to administration in vivo of the resulting recombinant cell. Such introduction can be carried out by any method

known in the art, including but not limited to transfection, electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the introduction of foreign genes 5 into cells (see, e.g., Loeffler and Behr, Meth. Enzymol. 217:599-618 (1993); Cohen et al., Meth. Enzymol. 217:618-644 (1993); Cline, Pharmac. Ther. 29:69-92m (1985) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is 10 expressible by the cell and preferably heritable and expressible by its cell progeny.

The resulting recombinant cells can be delivered to a patient by various methods known in the art. Recombinant blood cells (e.g., hematopoietic stem or progenitor cells) are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, patient state, etc., and can be determined by one skilled in the art.

15 Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include but are not limited to epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes; blood cells such as Tlymphocytes, Blymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, granulocytes; various stem or progenitor cells, in particular hematopoietic 20 stem or progenitor cells, e.g., as obtained from bone marrow, umbilical cord blood, peripheral blood, fetal liver, etc.

In a preferred embodiment, the cell used for gene therapy is autologous to the patient.

25 In an embodiment in which recombinant cells are used in gene therapy, nucleic acid sequences encoding an antibody are introduced into the cells such that they are expressible by the cells or their progeny, and the recombinant cells are then administered in vivo for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem and/or progenitor cells which can be isolated and maintained in vitro can potentially be used in accordance with this embodiment of the present invention (see e.g. PCT Publication WO 94/08598; Stemple and Anderson, Cell 71:973-985 (1992); Rheinwald, Meth. Cell Bio. 30 21A:229 (1980); and Pittelkow and Scott, Mayo Clinic Proc. 61:771 (1986)).

In a specific embodiment, the nucleic acid to be introduced for purposes of gene therapy comprises an inducible promoter operably linked to the coding region, such that

expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription. Demonstration of Therapeutic or Prophylactic Activity

The compounds or pharmaceutical compositions of the invention are preferably tested in vitro, and then in vivo for the desired therapeutic or prophylactic activity, prior to use in humans. For example, in vitro assays to demonstrate the therapeutic or prophylactic utility of a compound or pharmaceutical composition include, the effect of a compound on a cell line or a patient tissue sample. The effect of the compound or composition on the cell line and/or tissue sample can be determined utilizing techniques known to those of skill in the art including, but not limited to, rosette formation assays and cell lysis assays. In accordance with the invention, in vitro assays which can be used to determine whether administration of a specific compound is indicated, include in vitro cell culture assays in which a patient tissue sample is grown in culture, and exposed to or otherwise administered a compound, and the effect of such compound upon the tissue sample is observed.

15 *Therapeutic/Prophylactic Administration and Composition*

The invention provides methods of treatment, inhibition and prophylaxis by administration to a subject of an effective amount of a compound or pharmaceutical composition of the invention, preferably a polypeptide or antibody of the invention. In a preferred aspect, the compound is substantially purified (e.g., substantially free from substances that limit its effect or produce undesired side-effects). The subject is preferably an animal, including but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a mammal, and most preferably human.

Formulations and methods of administration that can be employed when the compound comprises a nucleic acid or an immunoglobulin are described above; additional appropriate formulations and routes of administration can be selected from among those described herein below.

Various delivery systems are known and can be used to administer a compound of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the compound, receptor-mediated endocytosis (see, e.g., Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987)), construction of a nucleic acid as part of a retroviral or other vector, etc. Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral

routes. The compounds or compositions may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, it may be desirable to introduce the pharmaceutical compounds or compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compounds or compositions of the invention locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. Preferably, when administering a protein, including an antibody, of the invention, care must be taken to use materials to which the protein does not absorb.

In another embodiment, the compound or composition can be delivered in a vesicle, in particular a liposome (see Langer, Science 249:1527-1533 (1990); Treat et al., in Liposomes in the Therapy of Infectious Disease and Cancer, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353- 365 (1989); Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*)

In yet another embodiment, the compound or composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, CRC Crit. Ref. Biomed. Eng. 14:201 (1987); Buchwald et al., Surgery 88:507 (1980); Saudek et al., N. Engl. J. Med. 321:574 (1989)). In another embodiment, polymeric materials can be used (see Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Pres., Boca Raton, Florida (1974); Controlled Drug Bioavailability, Drug Product Design and Performance, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, J., Macromol. Sci. Rev. Macromol. Chem. 23:61 (1983); see also Levy et al., Science 228:190 (1985); During et al., Ann. Neurol. 25:351 (1989); Howard et al.,

J.Neurosurg. 71:105 (1989)). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in Medical Applications of Controlled Release, *supra*, vol. 2, pp. 115-138 (1984)).

- 5 Other controlled release systems are discussed in the review by Langer (Science 249:1527-1533 (1990)).

In a specific embodiment where the compound of the invention is a nucleic acid encoding a protein, the nucleic acid can be administered *in vivo* to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic acid expression vector 10 and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (see U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (e.g.. a gene gun; Biostatic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox- like peptide which is known to enter the nucleus (see e.g., Joliot et al., Proc. Natl. Acad. Sci. USA 88:1864-1868 15 (1991)), etc. Alternatively, a nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination.

The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of a compound, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means 20 approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic 25 origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol 30 monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of

solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate,
5 sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the compound, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of
10 administration.

In a preferred embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing
15 agent and a local anesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent.
Where the composition is to be administered by infusion, it can be dispensed with an
20 infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

The compounds of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with anions such as those derived
25 from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with cations such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The amount of the compound of the invention which will be effective in the treatment, inhibition and prevention of a disease or disorder associated with aberrant
30 expression and/or activity of a polypeptide of the invention can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend

on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

5 For antibodies, the dosage administered to a patient is typically 0.1 mg/kg to 100 mg/kg of the patient's body weight. Preferably, the dosage administered to a patient is between 0.1 mg/kg and 20 mg/kg of the patient's body weight, more preferably 1 mg/kg to 10 mg/kg of the patient's body weight. Generally, human antibodies have a longer half-life within the human body than antibodies from other species due to the immune response to the
10 foreign polypeptides. Thus, lower dosages of human antibodies and less frequent administration is often possible. Further, the dosage and frequency of administration of antibodies of the invention may be reduced by enhancing uptake and tissue penetration (e.g., into the brain) of the antibodies by modifications such as, for example, lipidation.

15 The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

20

Diagnosis and Imaging

25 Labeled antibodies, and derivatives and analogs thereof, which specifically bind to a polypeptide of interest can be used for diagnostic purposes to detect, diagnose, or monitor diseases, disorders, and/or conditions associated with the aberrant expression and/or activity of a polypeptide of the invention. The invention provides for the detection of aberrant expression of a polypeptide of interest, comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide interest and (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide
30 gene expression level compared to the standard expression level is indicative of aberrant expression.

The invention provides a diagnostic assay for diagnosing a disorder, comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide interest and (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in 5 the assayed polypeptide gene expression level compared to the standard expression level is indicative of a particular disorder. With respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow 10 health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Antibodies of the invention can be used to assay protein levels in a biological sample using classical immunohistological methods known to those of skill in the art (e.g., see Jalkanen, et al., *J. Cell. Biol.* 101:976-985 (1985); Jalkanen, et al., *J. Cell. Biol.* 105:3087-15 3096 (1987)). Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase; radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and technetium (99Tc); luminescent labels, 20 such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

One aspect of the invention is the detection and diagnosis of a disease or disorder associated with aberrant expression of a polypeptide of interest in an animal, preferably a mammal and most preferably a human. In one embodiment, diagnosis comprises: a) administering (for example, parenterally, subcutaneously, or intraperitoneally) to a subject an 25 effective amount of a labeled molecule which specifically binds to the polypeptide of interest; b) waiting for a time interval following the administering for permitting the labeled molecule to preferentially concentrate at sites in the subject where the polypeptide is expressed (and for unbound labeled molecule to be cleared to background level); c) determining background level; and d) detecting the labeled molecule in the subject, such that 30 detection of labeled molecule above the background level indicates that the subject has a particular disease or disorder associated with aberrant expression of the polypeptide of interest. Background level can be determined by various methods including, comparing the

amount of labeled molecule detected to a standard value previously determined for a particular system.

It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the 5 case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of ^{99m}Tc . The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 10 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes. eds., Masson Publishing Inc. (1982).

Depending on several variables, including the type of label used and the mode of administration, the time interval following the administration for permitting the labeled molecule to preferentially concentrate at sites in the subject and for unbound labeled 15 molecule to be cleared to background level is 6 to 48 hours or 6 to 24 hours or 6 to 12 hours. In another embodiment the time interval following administration is 5 to 20 days or 5 to 10 days.

In an embodiment, monitoring of the disease or disorder is carried out by repeating the method for diagnosing the disease or disorder, for example, one month after initial 20 diagnosis, six months after initial diagnosis, one year after initial diagnosis, etc.

Presence of the labeled molecule can be detected in the patient using methods known in the art for in vivo scanning. These methods depend upon the type of label used. Skilled artisans will be able to determine the appropriate method for detecting a particular label. Methods and devices that may be used in the diagnostic methods of the invention include, but 25 are not limited to, computed tomography (CT), whole body scan such as position emission tomography (PET), magnetic resonance imaging (MRI), and sonography.

In a specific embodiment, the molecule is labeled with a radioisotope and is detected in the patient using a radiation responsive surgical instrument (Thurston et al., U.S. Patent No. 5,441,050). In another embodiment, the molecule is labeled with a fluorescent 30 compound and is detected in the patient using a fluorescence responsive scanning instrument. In another embodiment, the molecule is labeled with a positron emitting metal and is detected in the patient using positron emission-tomography. In yet another embodiment, the molecule

is labeled with a paramagnetic label and is detected in a patient using magnetic resonance imaging (MRI).

Kits

5 The present invention provides kits that can be used in the above methods. In one embodiment, a kit comprises an antibody of the invention, preferably a purified antibody, in one or more containers. In a specific embodiment, the kits of the present invention contain a substantially isolated polypeptide comprising an epitope which is specifically immunoreactive with an antibody included in the kit. Preferably, the kits of the present 10 invention further comprise a control antibody which does not react with the polypeptide of interest. In another specific embodiment, the kits of the present invention contain a means for detecting the binding of an antibody to a polypeptide of interest (e.g., the antibody may be conjugated to a detectable substrate such as a fluorescent compound, an enzymatic substrate, a radioactive compound or a luminescent compound, or a second antibody which recognizes 15 the first antibody may be conjugated to a detectable substrate).

In another specific embodiment of the present invention, the kit is a diagnostic kit for use in screening serum containing antibodies specific against proliferative and/or cancerous polynucleotides and polypeptides. Such a kit may include a control antibody that does not react with the polypeptide of interest. Such a kit may include a substantially isolated 20 polypeptide antigen comprising an epitope which is specifically immunoreactive with at least one anti-polypeptide antigen antibody. Further, such a kit includes means for detecting the binding of said antibody to the antigen (e.g., the antibody may be conjugated to a fluorescent compound such as fluorescein or rhodamine which can be detected by flow cytometry). In specific embodiments, the kit may include a recombinantly produced or chemically 25 synthesized polypeptide antigen. The polypeptide antigen of the kit may also be attached to a solid support.

In a more specific embodiment the detecting means of the above-described kit includes a solid support to which said polypeptide antigen is attached. Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of 30 the antibody to the polypeptide antigen can be detected by binding of the said reporter-labeled antibody.

In an additional embodiment, the invention includes a diagnostic kit for use in screening serum containing antigens of the polypeptide of the invention. The diagnostic kit includes a substantially isolated antibody specifically immunoreactive with polypeptide or polynucleotide antigens, and means for detecting the binding of the polynucleotide or polypeptide antigen to the antibody. In one embodiment, the antibody is attached to a solid support. In a specific embodiment, the antibody may be a monoclonal antibody. The detecting means of the kit may include a second, labeled monoclonal antibody. Alternatively, or in addition, the detecting means may include a labeled, competing antigen.

In one diagnostic configuration, test serum is reacted with a solid phase reagent having a surface-bound antigen obtained by the methods of the present invention. After binding with specific antigen antibody to the reagent and removing unbound serum components by washing, the reagent is reacted with reporter-labeled anti-human antibody to bind reporter to the reagent in proportion to the amount of bound anti-antigen antibody on the solid support. The reagent is again washed to remove unbound labeled antibody, and the amount of reporter associated with the reagent is determined. Typically, the reporter is an enzyme which is detected by incubating the solid phase in the presence of a suitable fluorometric, luminescent or colorimetric substrate (Sigma, St. Louis, MO).

The solid surface reagent in the above assay is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plate or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

Thus, the invention provides an assay system or kit for carrying out this diagnostic method. The kit generally includes a support with surface- bound recombinant antigens, and a reporter-labeled anti-human antibody for detecting surface-bound anti-antigen antibody.

Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The colon cancer antigen polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each sequence is specifically targeted to and can 5 hybridize with a particular location on an individual human chromosome, thus each polynucleotide of the present invention can routinely be used as a chromosome marker using techniques known in the art.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably at least 15 bp (e.g., 15-25 bp) from the sequences shown in SEQ ID NO:X, or the 10 complement thereto. Primers can optionally be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to SEQ ID NO:X will yield an amplified fragment.

15 Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted 20 chromosomes, preselection by hybridization to construct chromosome specific-cDNA libraries, and computer mapping techniques (See, e.g., Shuler, Trends Biotechnol 16:456-459 (1998) which is hereby incorporated by reference in its entirety).

Precise chromosomal location of the polynucleotides can also be achieved using 25 fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a 30 single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes).

Thus, the present invention also provides a method for chromosomal localization which involves (a) preparing PCR primers from the polynucleotide sequences in Table 3 and SEQ ID NO:X and (b) screening somatic cell hybrids containing individual chromosomes.

The polynucleotides of the present invention would likewise be useful for radiation hybrid mapping, HAPPY mapping, and long range restriction mapping. For a review of these techniques and others known in the art, see, e.g. Dear, "Genome Mapping: A Practical Approach," IRL Press at Oxford University Press, London (1997); Aydin, J. Mol. Med. 77:691-694 (1999); Hacia et al., Mol. Psychiatry 3:483-492 (1998); Herrick et al., Chromosome Res. 7:409-423 (1999); Hamilton et al., Methods Cell Biol. 62:265-280 (2000); 10 and/or Ott, J. Hered. 90:68-70 (1999) each of which is hereby incorporated by reference in its entirety.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage analysis establishes coinheritance between a chromosomal location and presentation of a particular 15 disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library).) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

20 Thus, once coinheritance is established, differences in a polynucleotide of the invention and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all 25 affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

30 Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using the polynucleotides of the

invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

Thus, the invention provides a method of detecting increased or decreased expression levels of the colon cancer polynucleotides in affected individuals as compared to unaffected individuals using polynucleotides of the present invention and techniques known in the art, including but not limited to the method described in Example 11. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

Thus, the invention also provides a diagnostic method useful during diagnosis of a colon related disorder, including colon cancer, involving measuring the expression level of colon cancer polynucleotides in colon tissue or other cells or body fluid from an individual and comparing the measured gene expression level with a standard colon cancer polynucleotide expression level, whereby an increase or decrease in the gene expression level compared to the standard is indicative of a colon related disorder.

In still another embodiment, the invention includes a kit for analyzing samples for the presence of proliferative and/or cancerous polynucleotides derived from a test subject. In a general embodiment, the kit includes at least one polynucleotide probe containing a nucleotide sequence that will specifically hybridize with a polynucleotide of the invention and a suitable container. In a specific embodiment, the kit includes two polynucleotide probes defining an internal region of the polynucleotide of the invention, where each probe has one strand containing a 31'mer-end internal to the region. In a further embodiment, the probes may be useful as primers for polymerase chain reaction amplification.

Where a diagnosis of a colon related disorder, including, for example, diagnosis of a tumor, has already been made according to conventional methods, the present invention is useful as a prognostic indicator, whereby patients exhibiting enhanced or depressed colon cancer polynucleotide expression will experience a worse clinical outcome relative to patients expressing the gene at a level nearer the standard level.

By "measuring the expression level of colon cancer polynucleotides" is intended qualitatively or quantitatively measuring or estimating the level of the colon cancer polypeptide or the level of the mRNA encoding the colon cancer polypeptide in a first biological sample either directly (e.g., by determining or estimating absolute protein level or mRNA level) or relatively (e.g., by comparing to the colon cancer polypeptide level or

mRNA level in a second biological sample). Preferably, the colon cancer polypeptide level or mRNA level in the first biological sample is measured or estimated and compared to a standard colon cancer polypeptide level or mRNA level, the standard being taken from a second biological sample obtained from an individual not having the colon related disorder or 5 being determined by averaging levels from a population of individuals not having a colon related disorder. As will be appreciated in the art, once a standard colon cancer polypeptide level or mRNA level is known, it can be used repeatedly as a standard for comparison.

By "biological sample" is intended any biological sample obtained from an individual, body fluid, cell line, tissue culture, or other source which contains colon cancer polypeptide 10 or the corresponding mRNA. As indicated, biological samples include body fluids (such as lymph, sera, plasma, urine, bile, synovial fluid and spinal fluid) which contain the colon cancer polypeptide, colon tissue, and other tissue sources found to express the colon cancer polypeptide. Methods for obtaining tissue biopsies and body fluids from mammals are well known in the art. Where the biological sample is to include mRNA, a tissue biopsy is the 15 preferred source.

The method(s) provided above may preferably be applied in a diagnostic method and/or kits in which polynucleotides and/or polypeptides of the invention are attached to a solid support. In one exemplary method, the support may be a "gene chip" or a "biological chip" as described in US Patents 5,837,832, 5,874,219, and 5,856,174. Further, such a gene 20 chip with colon cancer polynucleotides attached may be used to identify polymorphisms between the colon cancer polynucleotide sequences, with polynucleotides isolated from a test subject. The knowledge of such polymorphisms (i.e. their location, as well as, their existence) would be beneficial in identifying disease loci for many disorders, such as for example, in neural disorders, immune system disorders, muscular disorders, reproductive 25 disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders, and/or cancerous diseases and conditions, though most preferably in colon related proliferative, and/or cancerous diseases and conditions. Such a method is described in US Patents 5,858,659 and 5,856,104. The US Patents referenced supra are hereby incorporated by reference in their entirety herein.

30 The present invention encompasses colon cancer polynucleotides that are chemically synthesized, or reproduced as peptide nucleic acids (PNA), or according to other methods known in the art. The use of PNAs would serve as the preferred form if the polynucleotides

of the invention are incorporated onto a solid support, or gene chip. For the purposes of the present invention, a peptide nucleic acid (PNA) is a polyamide type of DNA analog and the monomeric units for adenine, guanine, thymine and cytosine are available commercially (Perceptive Biosystems). Certain components of DNA, such as phosphorus, phosphorus oxides, or deoxyribose derivatives, are not present in PNAs. As disclosed by P. E. Nielsen, M. Egholm, R. H. Berg and O. Buchardt, Science 254, 1497 (1991); and M. Egholm, O. Buchardt, L. Christensen, C. Behrens, S. M. Freier, D. A. Driver, R. H. Berg, S. K. Kim, B. Norden, and P. E. Nielsen, Nature 365, 666 (1993), PNAs bind specifically and tightly to complementary DNA strands and are not degraded by nucleases. In fact, PNA binds more strongly to DNA than DNA itself does. This is probably because there is no electrostatic repulsion between the two strands, and also the polyamide backbone is more flexible. Because of this, PNA/DNA duplexes bind under a wider range of stringency conditions than DNA/DNA duplexes, making it easier to perform multiplex hybridization. Smaller probes can be used than with DNA due to the strong binding. In addition, it is more likely that single base mismatches can be determined with PNA/DNA hybridization because a single mismatch in a PNA/DNA 15-mer lowers the melting point ($T_{\text{sub.m}}$) by 8° - 20° C, vs. 4° - 16° C for the DNA/DNA 15-mer duplex. Also, the absence of charge groups in PNA means that hybridization can be done at low ionic strengths and reduce possible interference by salt during the analysis.

The present invention have uses which include, but are not limited to, detecting cancer in mammals. In particular the invention is useful during diagnosis of pathological cell proliferative neoplasias which include, but are not limited to: acute myelogenous leukemias including acute monocytic leukemia, acute myeloblastic leukemia, acute promyelocytic leukemia, acute myelomonocytic leukemia, acute erythroleukemia, acute megakaryocytic leukemia, and acute undifferentiated leukemia, etc.; and chronic myelogenous leukemias including chronic myelomonocytic leukemia, chronic granulocytic leukemia, etc. Preferred mammals include monkeys, apes, cats, dogs, cows, pigs, horses, rabbits and humans. Particularly preferred are humans.

Pathological cell proliferative disorders are often associated with inappropriate activation of proto-oncogenes. (Gelmann, E. P. et al., "The Etiology of Acute Leukemia: Molecular Genetics and Viral Oncology," in *Neoplastic Diseases of the Blood*, Vol 1., Wiernik, P. H. et al. eds., 161-182 (1985)). Neoplasias are now believed to result from the

qualitative alteration of a normal cellular gene product, or from the quantitative modification of gene expression by insertion into the chromosome of a viral sequence, by chromosomal translocation of a gene to a more actively transcribed region, or by some other mechanism. (Gelmann et al., *supra*) It is likely that mutated or altered expression of specific genes is 5 involved in the pathogenesis of some leukemias, among other tissues and cell types. (Gelmann et al., *supra*) Indeed, the human counterparts of the oncogenes involved in some animal neoplasias have been amplified or translocated in some cases of human leukemia and carcinoma. (Gelmann et al., *supra*)

For example, c-myc expression is highly amplified in the non-lymphocytic leukemia 10 cell line HL-60. When HL-60 cells are chemically induced to stop proliferation, the level of c-myc is found to be downregulated. (International Publication Number WO 91/15580). However, it has been shown that exposure of HL-60 cells to a DNA construct that is complementary to the 5' end of c-myc or c-myb blocks translation of the corresponding 15 mRNAs which downregulates expression of the c-myc or c-myb proteins and causes arrest of cell proliferation and differentiation of the treated cells. (International Publication Number WO 91/15580; Wickstrom et al., Proc. Natl. Acad. Sci. 85:1028 (1988); Anfossi et al., Proc. Natl. Acad. Sci. 86:3379 (1989)). However, the skilled artisan would appreciate the present invention's usefulness is not limited to treatment of proliferative disorders of hematopoietic 20 cells and tissues, in light of the numerous cells and cell types of varying origins which are known to exhibit proliferative phenotypes.

In addition to the foregoing, a colon cancer antigen polynucleotide can be used to control gene expression through triple helix formation or through antisense DNA or RNA. Antisense techniques are discussed, for example, in Okano, J. Neurochem. 56: 560 (1991); "Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, 25 FL (1988). Triple helix formation is discussed in, for instance Lee et al., Nucleic Acids Research 6: 3073 (1979); Cooney et al., Science 241: 456 (1988); and Dervan et al., Science 251: 1360 (1991). Both methods rely on binding of the polynucleotide to a complementary DNA or RNA. For these techniques, preferred polynucleotides are usually oligonucleotides 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense 30

Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. The oligonucleotide described above can also be delivered to cells such that the antisense RNA or DNA may be 5 expressed in vivo to inhibit production of polypeptide of the present invention antigens. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease, and in particular, for the treatment of proliferative diseases and/or conditions.

Polynucleotides of the present invention are also useful in gene therapy. One goal of 10 gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

15 The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not 20 suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an 25 individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue 30 samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues,

e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, synovial fluid, amniotic fluid, breast milk, lymph, pulmonary sputum or surfactant, urine, fecal matter, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify
5 individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

10 There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to colon or colon cancer polynucleotides prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar
15 fashion, these reagents can be used to screen tissue cultures for contamination.

The polynucleotides of the present invention are also useful as hybridization probes for differential identification of the tissue(s) or cell type(s) present in a biological sample. Similarly, polypeptides and antibodies directed to polypeptides of the present invention are useful to provide immunological probes for differential identification of the tissue(s) (e.g.,
20 immunohistochemistry assays) or cell type(s) (e.g., immunocytochemistry assays). In addition, for a number of disorders of the above tissues or cells, significantly higher or lower levels of gene expression of the polynucleotides/polypeptides of the present invention may be detected in certain tissues (e.g., tissues expressing polypeptides and/or polynucleotides of the present invention, colon and colon cancer tissues and/or cancerous and/or wounded tissues)
25 or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) taken from an individual having such a disorder, relative to a "standard" gene expression level, i.e., the expression level in healthy tissue from an individual not having the disorder.

Thus, the invention provides a diagnostic method of a disorder, which involves: (a) assaying gene expression level in cells or body fluid of an individual; (b) comparing the gene
30 expression level with a standard gene expression level, whereby an increase or decrease in the assayed gene expression level compared to the standard expression level is indicative of a disorder.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

Polypeptides and antibodies directed to polypeptides of the present invention are useful to provide immunological probes for differential identification of the tissue(s) (e.g., immunohistochemistry assays such as, for example, ABC immunoperoxidase (Hsu et al., J. Histochem. Cytochem. 29:577-580 (1981)) or cell type(s) (e.g., immunocytochemistry assays).

Antibodies can be used to assay levels of polypeptides encoded by polynucleotides of the invention in a biological sample using classical immunohistological methods known to those of skill in the art (e.g., see Jalkanen, et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, et al., J. Cell. Biol. 105:3087-3096 (1987)). Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase; radioisotopes, such as iodine (¹³¹I, ¹²⁵I, ¹²³I, ¹²¹I), carbon (¹⁴C), sulfur (³⁵S), tritium (³H), indium (^{115m}In, ^{113m}In, ¹¹²In, ¹¹¹In), and technetium (⁹⁹Tc, ^{99m}Tc), thallium (²⁰¹Tl), gallium (⁶⁸Ga, ⁶⁷Ga), palladium (¹⁰³Pd), molybdenum (⁹⁹Mo), xenon (¹³³Xe), fluorine (¹⁸F), ¹⁵³Sm, ¹⁷⁷Lu, ¹⁵⁹Gd, ¹⁴⁹Pm, ¹⁴⁰La, ¹⁷⁵Yb, ¹⁶⁶Ho, ⁹⁰Y, ⁴⁷Sc, ¹⁸⁶Re, ¹⁸⁸Re, ¹⁴²Pr, ¹⁰⁵Rh, ⁹⁷Ru; luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying levels of polypeptide of the present invention in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit

detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, ^{131}I , ^{112}In , $^{99\text{m}}\text{Tc}$, (^{131}I , ^{125}I , ^{123}I , ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium ($^{115\text{m}}\text{In}$, $^{113\text{m}}\text{In}$, ^{112}In , ^{111}In), and technetium (^{99}Tc , $^{99\text{m}}\text{Tc}$), thallium (^{201}Tl), gallium (^{68}Ga , ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{18}F , ^{153}Sm , ^{177}Lu , ^{159}Gd , ^{149}Pm , ^{140}La , ^{175}Yb , ^{166}Ho , ^{90}Y , ^{47}Sc , ^{186}Re , ^{188}Re , ^{142}Pr , ^{105}Rh , ^{97}Ru), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously or intraperitoneally) into the mammal to be examined for immune system disorder. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of $^{99\text{m}}\text{Tc}$. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which express the polypeptide encoded by a polynucleotide of the invention. *In vivo* tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments" (Chapter 13 in *Tumor Imaging: The Radiochemical Detection of Cancer*, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982)).

In one embodiment, the invention provides a method for the specific delivery of compositions of the invention to cells by administering polypeptides of the invention (e.g., polypeptides encoded by polynucleotides of the invention and/or antibodies) that are associated with heterologous polypeptides or nucleic acids. In one example, the invention provides a method for delivering a therapeutic protein into the targeted cell. In another example, the invention provides a method for delivering a single stranded nucleic acid (e.g., antisense or ribozymes) or double stranded nucleic acid (e.g., DNA that can integrate into the cell's genome or replicate episomally and that can be transcribed) into the targeted cell.

In another embodiment, the invention provides a method for the specific destruction of cells (e.g.. the destruction of tumor cells) by administering polypeptides of the invention in association with toxins or cytotoxic prodrugs.

By "toxin" is meant one or more compounds that bind and activate endogenous cytotoxic effector systems, radioisotopes, holotoxins, modified toxins, catalytic subunits of toxins, or any molecules or enzymes not normally present in or on the surface of a cell that under defined conditions cause the cell's death. Toxins that may be used according to the methods of the invention include, but are not limited to, radioisotopes known in the art, compounds such as, for example, antibodies (or complement fixing containing portions thereof) that bind an inherent or induced endogenous cytotoxic effector system, thymidine kinase, endonuclease, RNase, alpha toxin, ricin, abrin, *Pseudomonas* exotoxin A, diphtheria toxin, saporin, momordin, gelonin, pokeweed antiviral protein, alpha-sarcin and cholera toxin. "Toxin" also includes a cytostatic or cytocidal agent, a therapeutic agent or a radioactive metal ion, e.g., alpha-emitters such as, for example, ²¹³Bi, or other radioisotopes such as, for example, ¹⁰³Pd, ¹³³Xe, ¹³¹I, ⁶⁸Ge, ⁵⁷Co, ⁶⁵Zn, ⁸⁵Sr, ³²P, ³⁵S, ⁹⁰Y, ¹⁵³Sm, ¹⁵³Gd, ¹⁶⁹Yb, ⁵¹Cr, ⁵⁴Mn, ⁷⁵Se, ¹¹³Sn, ⁹⁰Yttrium, ¹¹⁷Tin, ¹⁸⁶Rhenium, ¹⁶⁶Holmium, and ¹⁸⁸Rhenium; luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Techniques known in the art may be applied to label polypeptides of the invention (including antibodies). Such techniques include, but are not limited to, the use of bifunctional conjugating agents (see e.g., U.S. Patent Nos. 5,756,065; 5,714,631; 5,696,239; 5,652,361; 5,505,931; 5,489,425; 5,435,990; 5,428,139; 5,342,604; 5,274,119; 4,994,560; and 5,808,003; the contents of each of which are hereby incorporated by reference in its entirety).

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression level of a colon cancer polypeptide of the present invention in cells or body fluid of an individual, or more preferably, assaying the expression level of a colon cancer polypeptide of the present invention in colon cells or sera of an individual; and (b) comparing the assayed polypeptide expression level with a standard polypeptide expression level, whereby an increase or decrease in the assayed polypeptide expression level compared to the standard expression level is indicative of a disorder. With respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or

aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Moreover, colon cancer antigen polypeptides of the present invention can be used to treat or prevent diseases or conditions such as, for example, neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders, and/or cancerous diseases and conditions, preferably proliferative disorders of the colon, and/or cancerous disease and conditions. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B, SOD, catalase, DNA repair proteins), to inhibit the activity of a polypeptide (e.g., an oncogene or tumor suppressor), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth inhibition, enhancement of the immune response to proliferative cells or tissues).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease (as described supra, and elsewhere herein). For example, administration of an antibody directed to a polypeptide of the present invention can bind, and/or neutralize the polypeptide, and/or reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Gene Therapy Methods

Another aspect of the present invention is to gene therapy methods for treating or preventing disorders, diseases and conditions. The gene therapy methods relate to the introduction of nucleic acid (DNA, RNA and antisense DNA or RNA) sequences into an animal to achieve expression of the polypeptide of the present invention. This method requires a polynucleotide which codes for a polypeptide of the present invention operatively linked to a promoter and any other genetic elements necessary for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques are known in the art, see, for example, WO90/11092, which is herein incorporated by reference.

Thus, for example, cells from a patient may be engineered with a polynucleotide (DNA or RNA) comprising a promoter operably linked to a polynucleotide of the present invention ex vivo, with the engineered cells then being provided to a patient to be treated with the polypeptide of the present invention. Such methods are well-known in the art. For example, see Belldegrun, A., et al., J. Natl. Cancer Inst. 85: 207-216 (1993); Ferrantini, M. et al., Cancer Research 53: 1107-1112 (1993); Ferrantini, M. et al., J. Immunology 153: 4604-4615 (1994); Kaido, T., et al., Int. J. Cancer 60: 221-229 (1995); Ogura, H., et al., Cancer Research 50: 5102-5106 (1990); Santodonato, L., et al., Human Gene Therapy 7:1-10 (1996); Santodonato, L., et al., Gene Therapy 4:1246-1255 (1997); and Zhang, J.-F. et al., Cancer Gene Therapy 3: 31-38 (1996)), which are herein incorporated by reference. In one embodiment, the cells which are engineered are arterial cells. The arterial cells may be reintroduced into the patient through direct injection to the artery, the tissues surrounding the artery, or through catheter injection.

As discussed in more detail below, the polynucleotide constructs can be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, and the like). The polynucleotide constructs may be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

In one embodiment, the polynucleotide of the present invention is delivered as a naked polynucleotide. The term "naked" polynucleotide, DNA or RNA refers to sequences that are free from any delivery vehicle that acts to assist, promote or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotide of the present invention can

also be delivered in liposome formulations and lipofectin formulations and the like can be prepared by methods well known to those skilled in the art. Such methods are described, for example, in U.S. Patent Nos. 5,593,972, 5,589,466, and 5,580,859, which are herein incorporated by reference.

5 The polynucleotide vector constructs used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Appropriate vectors include pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; pSVK3, pBPV, pMSG and pSVL available from Pharmacia; and pEF1/V5, pcDNA3.1, and pRc/CMV2 available from Invitrogen. Other suitable vectors
10 will be readily apparent to the skilled artisan.

Any strong promoter known to those skilled in the art can be used for driving the expression of the polynucleotide sequence. Suitable promoters include adenoviral promoters, such as the adenoviral major late promoter; or heterologous promoters, such as the cytomegalovirus (CMV) promoter; the respiratory syncytial virus (RSV) promoter; inducible
15 promoters, such as the MMT promoter, the metallothionein promoter; heat shock promoters; the albumin promoter; the ApoAI promoter; human globin promoters; viral thymidine kinase promoters, such as the Herpes Simplex thymidine kinase promoter; retroviral LTRs; the b-actin promoter; and human growth hormone promoters. The promoter also may be the native promoter for the polynucleotide of the present invention.

20 Unlike other gene therapy techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

The polynucleotide construct can be delivered to the interstitial space of tissues within
25 the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular, fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of
30 fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is

preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, 5 stem cells of blood or skin fibroblasts. In vivo muscle cells are particularly competent in their ability to take up and express polynucleotides.

For the naked nucleic acid sequence injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 mg/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more 10 preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration.

The preferred route of administration is by the parenteral route of injection into the 15 interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked DNA constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The naked polynucleotides are delivered by any method known in the art, including, 20 but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, and so-called "gene guns". These delivery methods are known in the art.

The constructs may also be delivered with delivery vehicles such as viral sequences, 25 viral particles, liposome formulations, lipofectin, precipitating agents, etc. Such methods of delivery are known in the art.

In certain embodiments, the polynucleotide constructs are complexed in a liposome preparation. Liposomal preparations for use in the instant invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. However, cationic liposomes are particularly preferred because a tight charge complex can be formed 30 between the cationic liposome and the polyanionic nucleic acid. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner et al., Proc. Natl. Acad. Sci. USA (1987) 84:7413-7416, which is herein incorporated by reference); mRNA

(Malone et al., Proc. Natl. Acad. Sci. USA (1989) 86:6077-6081, which is herein incorporated by reference); and purified transcription factors (Debs et al., J. Biol. Chem. (1990) 265:10189-10192, which is herein incorporated by reference), in functional form.

- Cationic liposomes are readily available. For example,
- 5 N[1-2,3-dioleyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are particularly useful and are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, N.Y. (See, also, Felgner et al., Proc. Natl. Acad. Sci. USA (1987) 84:7413-7416, which is herein incorporated by reference). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer).
- 10 Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, e.g. PCT Publication No. WO 90/11092 (which is herein incorporated by reference) for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes. Preparation of DOTMA liposomes is explained in the literature, see, e.g., P. Felgner et al., Proc. Natl. Acad. Sci. USA 15 84:7413-7417, which is herein incorporated by reference. Similar methods can be used to prepare liposomes from other cationic lipid materials.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, Ala.), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, 20 dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

For example, commercially dioleoylphosphatidyl choline (DOPC), 25 dioleoylphosphatidyl glycerol (DOPG), and dioleoylphosphatidyl ethanolamine (DOPE) can be used in various combinations to make conventional liposomes, with or without the addition of cholesterol. Thus, for example, DOPG/DOPC vesicles can be prepared by drying 50 mg each of DOPG and DOPC under a stream of nitrogen gas into a sonication vial. The sample is placed under a vacuum pump overnight and is hydrated the following day with 30 deionized water. The sample is then sonicated for 2 hours in a capped vial, using a Heat Systems model 350 sonicator equipped with an inverted cup (bath type) probe at the maximum setting while the bath is circulated at 15EC. Alternatively, negatively charged

vesicles can be prepared without sonication to produce multilamellar vesicles or by extrusion through nucleopore membranes to produce unilamellar vesicles of discrete size. Other methods are known and available to those of skill in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs), with SUVs being preferred. The various liposome-nucleic acid complexes are prepared using methods well known in the art. See, e.g., Straubinger et al., *Méthodes of Immunology* (1983), 101:512-527, which is herein incorporated by reference. For example, MLVs containing nucleic acid can be prepared by depositing a thin film of phospholipid on the walls of a glass tube and subsequently hydrating with a solution of the material to be encapsulated. SUVs are prepared by extended sonication of MLVs to produce a homogeneous population of unilamellar liposomes. The material to be entrapped is added to a suspension of preformed MLVs and then sonicated. When using liposomes containing cationic lipids, the dried lipid film is resuspended in an appropriate solution such as sterile water or an isotonic buffer solution such as 10 mM Tris/NaCl, sonicated, and then the preformed liposomes are mixed directly with the DNA. The liposome and DNA form a very stable complex due to binding of the positively charged liposomes to the cationic DNA. SUVs find use with small nucleic acid fragments. LUVs are prepared by a number of methods, well known in the art. Commonly used methods include Ca^{2+} -EDTA chelation (Papahadjopoulos et al., *Biochim. Biophys. Acta* (1975) 394:483; Wilson et al., *Cell* (1979) 17:77); ether injection (Deamer, D. and Bangham, A., *Biochim. Biophys. Acta* (1976) 443:629; Ostro et al., *Biochem. Biophys. Res. Commun.* (1977) 76:836; Fraley et al., *Proc. Natl. Acad. Sci. USA* (1979) 76:3348); detergent dialysis (Enoch, H. and Strittmatter, P., *Proc. Natl. Acad. Sci. USA* (1979) 76:145); and reverse-phase evaporation (REV) (Fraley et al., *J. Biol. Chem.* (1980) 255:10431; Szoka, F. and Papahadjopoulos, D., *Proc. Natl. Acad. Sci. USA* (1978) 75:145; Schaefer-Ridder et al., *Science* (1982) 215:166), which are herein incorporated by reference.

Generally, the ratio of DNA to liposomes will be from about 10:1 to about 1:10. Preferably, the ration will be from about 5:1 to about 1:5. More preferably, the ration will be about 3:1 to about 1:3. Still more preferably, the ratio will be about 1:1.

U.S. Patent No. 5,676,954 (which is herein incorporated by reference) reports on the injection of genetic material, complexed with cationic liposomes carriers, into mice. U.S. Patent Nos. 4,897,355, 4,946,787, 5,049,386, 5,459,127, 5,589,466, 5,693,622, 5,580,859,

5.703.055, and international publication no. WO 94/9469 (which are herein incorporated by reference) provide cationic lipids for use in transfecting DNA into cells and mammals. U.S. Patent Nos. 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication no. WO 94/9469 (which are herein incorporated by reference) provide methods for delivering 5 DNA-cationic lipid complexes to mammals.

In certain embodiments, cells are engineered, ex vivo or in vivo, using a retroviral particle containing RNA which comprises a sequence encoding a polypeptide of the present invention. Retroviruses from which the retroviral plasmid vectors may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, Rous sarcoma 10 Virus, Harvey Sarcoma Virus, avian leukosis virus, gibbon ape leukemia virus, human immunodeficiency virus, Myeloproliferative Sarcoma Virus, and mammary tumor virus.

The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transfected include, but are not limited to, the PE501, PA317, R-2, R-AM, PA12, T19-14X, VT-19-17-H2, RCRE, 15 RCRIP, GP+E-86, GP+envAm12, and DAN cell lines as described in Miller, Human Gene Therapy 1:5-14 (1990), which is incorporated herein by reference in its entirety. The vector may transduce the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation, the use of liposomes, and CaPO₄ precipitation. In one alternative, the retroviral plasmid vector may be encapsulated into a liposome, or coupled to a 20 lipid, and then administered to a host.

The producer cell line generates infectious retroviral vector particles which include polynucleotide encoding a polypeptide of the present invention. Such retroviral vector particles then may be employed, to transduce eukaryotic cells, either in vitro or in vivo. The transduced eukaryotic cells will express a polypeptide of the present invention.

25 In certain other embodiments, cells are engineered, ex vivo or in vivo, with polynucleotide contained in an adenovirus vector. Adenovirus can be manipulated such that it encodes and expresses a polypeptide of the present invention, and at the same time is inactivated in terms of its ability to replicate in a normal lytic viral life cycle. Adenovirus expression is achieved without integration of the viral DNA into the host cell chromosome, 30 thereby alleviating concerns about insertional mutagenesis. Furthermore, adenoviruses have been used as live enteric vaccines for many years with an excellent safety profile (Schwartz, A. R. et al. (1974) Am. Rev. Respir. Dis. 109:233-238). Finally, adenovirus mediated gene

transfer has been demonstrated in a number of instances including transfer of alpha-1-antitrypsin and CFTR to the lungs of cotton rats (Rosenfeld, M. A. et al. (1991) Science 252:431-434; Rosenfeld et al., (1992) Cell 68:143-155). Furthermore, extensive studies to attempt to establish adenovirus as a causative agent in human cancer were 5 uniformly negative (Green, M. et al. (1979) Proc. Natl. Acad. Sci. USA 76:6606).

Suitable adenoviral vectors useful in the present invention are described, for example, in Kozarsky and Wilson, Curr. Opin. Genet. Devel. 3:499-503 (1993); Rosenfeld et al., Cell 68:143-155 (1992); Engelhardt et al., Human Genet. Ther. 4:759-769 (1993); Yang et al., Nature Genet. 7:362-369 (1994); Wilson et al., Nature 365:691-692 (1993); and U.S. Patent 10 No. 5,652,224, which are herein incorporated by reference. For example, the adenovirus vector Ad2 is useful and can be grown in human 293 cells. These cells contain the E1 region of adenovirus and constitutively express Ela and Elb, which complement the defective adenoviruses by providing the products of the genes deleted from the vector. In addition to Ad2, other varieties of adenovirus (e.g., Ad3, Ad5, and Ad7) are also useful in the present 15 invention.

Preferably, the adenoviruses used in the present invention are replication deficient. Replication deficient adenoviruses require the aid of a helper virus and/or packaging cell line to form infectious particles. The resulting virus is capable of infecting cells and can express a polynucleotide of interest which is operably linked to a promoter, but cannot replicate in most 20 cells. Replication deficient adenoviruses may be deleted in one or more of all or a portion of the following genes: Ela, Elb, E3, E4, E2a, or L1 through L5.

In certain other embodiments, the cells are engineered, ex vivo or in vivo, using an adeno-associated virus (AAV). AAVs are naturally occurring defective viruses that require helper viruses to produce infectious particles (Muzyczka, N., Curr. Topics in Microbiol. 25 Immunol. 158:97 (1992)). It is also one of the few viruses that may integrate its DNA into non-dividing cells. Vectors containing as little as 300 base pairs of AAV can be packaged and can integrate, but space for exogenous DNA is limited to about 4.5 kb. Methods for producing and using such AAVs are known in the art. See, for example, U.S. Patent Nos. 5,139,941, 5,173,414, 5,354,678, 5,436,146, 5,474,935, 5,478,745, and 5,589,377.

30 For example, an appropriate AAV vector for use in the present invention will include all the sequences necessary for DNA replication, encapsidation, and host-cell integration. The polynucleotide construct is inserted into the AAV vector using standard cloning

methods, such as those found in Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press (1989). The recombinant AAV vector is then transfected into packaging cells which are infected with a helper virus, using any standard technique, including lipofection, electroporation, calcium phosphate precipitation, etc. Appropriate 5 helper viruses include adenoviruses, cytomegaloviruses, vaccinia viruses, or herpes viruses. Once the packaging cells are transfected and infected, they will produce infectious AAV viral particles which contain the polynucleotide construct. These viral particles are then used to transduce eukaryotic cells, either ex vivo or in vivo. The transduced cells will contain the polynucleotide construct integrated into its genome, and will express a polypeptide of the 10 invention.

Another method of gene therapy involves operably associating heterologous control regions and endogenous polynucleotide sequences (e.g. encoding a polypeptide of the present invention) via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996; 15 International Publication No. WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989)). This method involves the activation of a gene which is present in the target cells, but which is not normally expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made, using standard techniques known in the art, 20 which contain the promoter with targeting sequences flanking the promoter. Suitable promoters are described herein. The targeting sequence is sufficiently complementary to an endogenous sequence to permit homologous recombination of the promoter-targeting sequence with the endogenous sequence. The targeting sequence will be sufficiently near the 5' end of the desired endogenous polynucleotide sequence so the promoter will be operably 25 linked to the endogenous sequence upon homologous recombination..

The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence 30 contains the same restriction site as the 3' end of the amplified promoter. The amplified promoter and targeting sequences are digested and ligated together.

The promoter-targeting sequence construct is delivered to the cells, either as naked polynucleotide, or in conjunction with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, whole viruses, lipofection, precipitating agents, etc., described in more detail above. The P promoter-targeting sequence can be delivered by any method, 5 included direct needle injection, intravenous injection, topical administration, catheter infusion, particle accelerators, etc. The methods are described in more detail below.

The promoter-targeting sequence construct is taken up by cells. Homologous recombination between the construct and the endogenous sequence takes place, such that an endogenous sequence is placed under the control of the promoter. The promoter then drives 10 the expression of the endogenous sequence.

Preferably, the polynucleotide encoding a polypeptide of the present invention contains a secretory signal sequence that facilitates secretion of the protein. Typically, the signal sequence is positioned in the coding region of the polynucleotide to be expressed towards or at the 5' end of the coding region. The signal sequence may be homologous or 15 heterologous to the polynucleotide of interest and may be homologous or heterologous to the cells to be transfected. Additionally, the signal sequence may be chemically synthesized using methods known in the art.

Any mode of administration of any of the above-described polynucleotides constructs can be used so long as the mode results in the expression of one or more molecules in an 20 amount sufficient to provide a therapeutic effect. This includes direct needle injection, systemic injection, catheter infusion, biostatic injectors, particle accelerators (i.e., "gene guns"), gelfoam sponge depots, other commercially available depot materials, osmotic pumps (e.g., Alza minipumps), oral or suppositorial solid (tablet or pill) pharmaceutical formulations, and decanting or topical applications during surgery. For example, direct 25 injection of naked calcium phosphate-precipitated plasmid into rat liver and rat spleen or a protein-coated plasmid into the portal vein has resulted in gene expression of the foreign gene in the rat livers (Kaneda et al., Science 243:375 (1989)).

A preferred method of local administration is by direct injection. Preferably, a recombinant molecule of the present invention complexed with a delivery vehicle is 30 administered by direct injection into or locally within the area of arteries. Administration of a composition locally within the area of arteries refers to injecting the composition centimeters and preferably, millimeters within arteries.

Another method of local administration is to contact a polynucleotide construct of the present invention in or around a surgical wound. For example, a patient can undergo surgery and the polynucleotide construct can be coated on the surface of tissue inside the wound or the construct can be injected into areas of tissue inside the wound.

5 Therapeutic compositions useful in systemic administration, include recombinant molecules of the present invention complexed to a targeted delivery vehicle of the present invention. Suitable delivery vehicles for use with systemic administration comprise liposomes comprising ligands for targeting the vehicle to a particular site.

Preferred methods of systemic administration, include intravenous injection, aerosol, 10 oral and percutaneous (topical) delivery. Intravenous injections can be performed using methods standard in the art. Aerosol delivery can also be performed using methods standard in the art (see, for example, Stribling et al., Proc. Natl. Acad. Sci. USA 89:11277-11281, 1992, which is incorporated herein by reference). Oral delivery can be performed by complexing a polynucleotide construct of the present invention to a carrier capable of 15 withstanding degradation by digestive enzymes in the gut of an animal. Examples of such carriers, include plastic capsules or tablets, such as those known in the art. Topical delivery can be performed by mixing a polynucleotide construct of the present invention with a lipophilic reagent (e.g., DMSO) that is capable of passing into the skin.

Determining an effective amount of substance to be delivered can depend upon a 20 number of factors including, for example, the chemical structure and biological activity of the substance, the age and weight of the animal, the precise condition requiring treatment and its severity, and the route of administration. The frequency of treatments depends upon a number of factors, such as the amount of polynucleotide constructs administered per dose, as well as the health and history of the subject. The precise amount, number of doses, and 25 timing of doses will be determined by the attending physician or veterinarian.

Therapeutic compositions of the present invention can be administered to any animal, preferably to mammals and birds. Preferred mammals include humans, dogs, cats, mice, rats, rabbits sheep, cattle, horses and pigs, with humans being particularly preferred.

30 **Biological Activities**

Polynucleotides or polypeptides, or agonists or antagonists of the present invention, can be used in assays to test for one or more biological activities. If these polynucleotides or

polypeptides, or agonists or antagonists of the present invention, do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides, and agonists or antagonists could be used to treat the associated disease.

5

Immune Activity

A polypeptide or polynucleotide, or agonists or antagonists of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells.

- 10 Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, polynucleotides or polypeptides, or
15 agonists or antagonists of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

- Polynucleotides or polypeptides, or agonists or antagonists of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. Polynucleotides or polypeptides, or agonists or antagonists of the present invention could be
20 used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable
25 immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

- Moreover, polynucleotides or polypeptides, or agonists or antagonists of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, polynucleotides or polypeptides, or agonists or antagonists of the

present invention could be used to treat blood coagulation disorders (e.g.. afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, polynucleotides or polypeptides, or agonists or antagonists of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of polynucleotides or polypeptides, or agonists or antagonists of the present invention that can inhibit an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by polynucleotides or polypeptides, or agonists or antagonists of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of

polynucleotides or polypeptides, or agonists or antagonists of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be used to modulate inflammation. For example, polynucleotides or polypeptides, or agonists or antagonists of the present invention may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including chronic prostatitis, granulomatous prostatitis and malacoplakia, inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.).

15 **Hyperproliferative Disorders**

Polynucleotides or polypeptides, or agonists or antagonists of the present invention can be used to treat or detect hyperproliferative disorders, including neoplasms. Polynucleotides or polypeptides, or agonists or antagonists of the present invention may inhibit the proliferation of the disorder through direct or indirect interactions. Alternatively, 20 Polynucleotides or polypeptides, or agonists or antagonists of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased 25 by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by Polynucleotides or polypeptides, or agonists or antagonists of the present invention include, 30 but are not limited to neoplasms located in the: colon, abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary,

testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by polynucleotides or polypeptides, or agonists or antagonists of the present invention.

5 Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

10 One preferred embodiment utilizes polynucleotides of the present invention to inhibit aberrant cellular division, by gene therapy using the present invention, and/or protein fusions or fragments thereof.

Thus, the present invention provides a method for treating cell proliferative disorders by inserting into an abnormally proliferating cell a polynucleotide of the present invention, 15 wherein said polynucleotide represses said expression.

Another embodiment of the present invention provides a method of treating cell-proliferative disorders in individuals comprising administration of one or more active gene copies of the present invention to an abnormally proliferating cell or cells. In a preferred embodiment, polynucleotides of the present invention is a DNA construct comprising a 20 recombinant expression vector effective in expressing a DNA sequence encoding said polynucleotides. In another preferred embodiment of the present invention, the DNA construct encoding the polynucleotides of the present invention is inserted into cells to be treated utilizing a retrovirus, or more preferably an adenoviral vector (See G J. Nabel, et. al., PNAS 1999 96: 324-326, which is hereby incorporated by reference). In a most preferred 25 embodiment, the viral vector is defective and will not transform non-proliferating cells, only proliferating cells. Moreover, in a preferred embodiment, the polynucleotides of the present invention inserted into proliferating cells either alone, or in combination with or fused to other polynucleotides, can then be modulated via an external stimulus (i.e. magnetic, specific small molecule, chemical, or drug administration, etc.), which acts upon the promoter 30 upstream of said polynucleotides to induce expression of the encoded protein product. As such the beneficial therapeutic affect of the present invention may be expressly modulated

(i.e. to increase, decrease, or inhibit expression of the present invention) based upon said external stimulus.

Polynucleotides of the present invention may be useful in repressing expression of oncogenic genes or antigens. By "repressing expression of the oncogenic genes" is intended 5 the suppression of the transcription of the gene, the degradation of the gene transcript (pre-messenger RNA), the inhibition of splicing, the destruction of the messenger RNA, the prevention of the post-translational modifications of the protein, the destruction of the protein, or the inhibition of the normal function of the protein.

For local administration to abnormally proliferating cells, polynucleotides of the 10 present invention may be administered by any method known to those of skill in the art including, but not limited to transfection, electroporation, microinjection of cells, or in vehicles such as liposomes, lipofectin, or as naked polynucleotides, or any other method described throughout the specification. The polynucleotide of the present invention may be delivered by known gene delivery systems such as, but not limited to, retroviral vectors 15 (Gilboa, J. Virology 44:845 (1982); Hocke, Nature 320:275 (1986); Wilson, et al., Proc. Natl. Acad. Sci. U.S.A. 85:3014), vaccinia virus system (Chakrabarty et al., Mol. Cell Biol. 5:3403 (1985) or other efficient DNA delivery systems (Yates et al., Nature 313:812 (1985)) known to those skilled in the art. These references are exemplary only and are hereby incorporated by reference. In order to specifically deliver or transfet cells which are abnormally 20 proliferating and spare non-dividing cells, it is preferable to utilize a retrovirus, or adenoviral (as described in the art and elsewhere herein) delivery system known to those of skill in the art. Since host DNA replication is required for retroviral DNA to integrate and the retrovirus will be unable to self replicate due to the lack of the retrovirus genes needed for its life cycle. Utilizing such a retroviral delivery system for polynucleotides of the present invention will 25 target said gene and constructs to abnormally proliferating cells and will spare the non-dividing normal cells.

The polynucleotides of the present invention may be delivered directly to cell proliferative disorder/disease sites in internal organs, body cavities and the like by use of imaging devices used to guide an injecting needle directly to the disease site. The 30 polynucleotides of the present invention may also be administered to disease sites at the time of surgical intervention.

By "cell proliferative disease" is meant any human or animal disease or disorder, affecting any one or any combination of organs, cavities, or body parts, which is characterized by single or multiple local abnormal proliferations of cells, groups of cells, or tissues, whether benign or malignant.

- 5 Any amount of the polynucleotides of the present invention may be administered as long as it has a biologically inhibiting effect on the proliferation of the treated cells. Moreover, it is possible to administer more than one of the polynucleotide of the present invention simultaneously to the same site. By "biologically inhibiting" is meant partial or total growth inhibition as well as decreases in the rate of proliferation or growth of the cells.
- 10 The biologically inhibitory dose may be determined by assessing the effects of the polynucleotides of the present invention on target malignant or abnormally proliferating cell growth in tissue culture, tumor growth in animals and cell cultures, or any other method known to one of ordinary skill in the art.

The present invention is further directed to antibody-based therapies which involve 15 administering of anti-polypeptides and anti-polynucleotide antibodies to a mammalian, preferably human, patient for treating one or more of the described disorders. Methods for producing anti-polypeptides and anti-polynucleotide antibodies polyclonal and monoclonal antibodies are described in detail elsewhere herein. Such antibodies may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

20 A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present invention locally or systemically in the body or by direct cytotoxicity of the antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the 25 art will know how to use the antibodies of the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

In particular, the antibodies, fragments and derivatives of the present invention are 30 useful for treating a subject having or developing cell proliferative and/or differentiation disorders as described herein. Such treatment comprises administering a single or multiple doses of the antibody, or a fragment, derivative, or a conjugate thereof.

The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth

factors, for example., which serve to increase the number or activity of effector cells which interact with the antibodies.

It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and therapy of disorders related to polynucleotides or polypeptides, including fragement thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for polynucleotides or polypeptides, including fragement thereof. Preferred binding affinities include those with a dissociation constant or Kd less than 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7} M, 5×10^{-8} M, 10^{-8} M, 10 5 $\times 10^{-9}$ M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10^{-15} M, and 10^{-15} M.

Moreover, polypeptides of the present invention are useful in inhibiting the angiogenesis of proliferative cells or tissues, either alone, as a protein fusion, or in combination with other polypeptides directly or indirectly, as described elsewhere herein. In a 15 most preferred embodiment, said anti-angiogenesis effect may be achieved indirectly, for example, through the inhibition of hematopoietic, tumor-specific cells, such as tumor-associated macrophages (See Joseph IB, et al. J Natl Cancer Inst, 90(21):1648-53 (1998), which is hereby incorporated by reference). Antibodies directed to polypeptides or polynucleotides of the present invention may also result in inhibition of angiogenesis directly, 20 or indirectly (See Witte L, et al., Cancer Metastasis Rev. 17(2):155-61 (1998), which is hereby incorporated by reference)).

Polypeptides, including protein fusions, of the present invention, or fragments thereof 25 may be useful in inhibiting proliferative cells or tissues through the induction of apoptosis. Said polypeptides may act either directly, or indirectly to induce apoptosis of proliferative cells and tissues, for example in the activation of a death-domain receptor, such as tumor necrosis factor (TNF) receptor-1, CD95 (Fas/APO-1), TNF-receptor-related apoptosis-mediated protein (TRAMP) and TNF-related apoptosis-inducing ligand (TRAIL) receptor-1 and -2 (See Schulze-Osthoff K, et.al., Eur J Biochem 254(3):439-59 (1998), which is hereby incorporated by reference). Moreover, in another preferred embodiment of the present 30 invention, said polypeptides may induce apoptosis through other mechanisms, such as in the activation of other proteins which will activate apoptosis, or through stimulating the expression of said proteins, either alone or in combination with small molecule drugs or

adjuvants, such as apoptonin, galectins, thioredoxins, antiinflammatory proteins (See for example, Mutat Res 400(1-2):447-55 (1998), Med Hypotheses.50(5):423-33 (1998), Chem Biol Interact. Apr 24;111-112:23-34 (1998), J Mol Med.76(6):402-12 (1998), Int J Tissue React;20(1):3-15 (1998), which are all hereby incorporated by reference).

- 5 Polypeptides, including protein fusions to, or fragments thereof, of the present invention are useful in inhibiting the metastasis of proliferative cells or tissues. Inhibition may occur as a direct result of administering polypeptides, or antibodies directed to said polypeptides as described elsewhere herein, or indirectly, such as activating the expression of proteins known to inhibit metastasis, for example alpha 4 integrins, (See, e.g., Curr Top 10 Microbiol Immunol 1998;231:125-41, which is hereby incorporated by reference). Such therapeutic affects of the present invention may be achieved either alone, or in combination with small molecule drugs or adjuvants.

In another embodiment, the invention provides a method of delivering compositions containing the polypeptides of the invention (e.g., compositions containing polypeptides or 15 polypeptide antibodies associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs) to targeted cells expressing the polypeptide of the present invention. Polypeptides or polypeptide antibodies of the invention may be associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions. Polypeptides, protein fusions to, or 20 fragments thereof, of the present invention are useful in enhancing the immunogenicity and/or antigenicity of proliferating cells or tissues, either directly, such as would occur if the polypeptides of the present invention 'vaccinated' the immune response to respond to proliferative antigens and immunogens, or indirectly, such as in activating the expression of proteins known to enhance the immune response (e.g. chemokines), to said antigens and 25 immunogens.

Cardiovascular Disorders

Polynucleotides or polypeptides, or agonists or antagonists of the present invention, may be used to treat cardiovascular disorders, including peripheral artery disease, such as 30 limb ischemia.

Cardiovascular disorders include cardiovascular abnormalities, such as arterio-arterial fistula, arteriovenous fistula, cerebral arteriovenous malformations, congenital heart defects,

pulmonary atresia, and Scimitar Syndrome. Congenital heart defects include aortic coarctation, cor triatriatum, coronary vessel anomalies, crisscross heart, dextrocardia, patent ductus arteriosus, Ebstein's anomaly, Eisenmenger complex, hypoplastic left heart syndrome, levocardia, tetralogy of fallot, transposition of great vessels, double outlet right ventricle, 5 tricuspid atresia, persistent truncus arteriosus, and heart septal defects, such as aortopulmonary septal defect, endocardial cushion defects, Lutembacher's Syndrome, trilogy of Fallot, ventricular heart septal defects.

Cardiovascular disorders also include heart disease, such as arrhythmias, carcinoid heart disease, high cardiac output, low cardiac output, cardiac tamponade, endocarditis 10 (including bacterial), heart aneurysm, cardiac arrest, congestive heart failure, congestive cardiomyopathy, paroxysmal dyspnea, cardiac edema, heart hypertrophy, congestive cardiomyopathy, left ventricular hypertrophy, right ventricular hypertrophy, post-infarction heart rupture, ventricular septal rupture, heart valve diseases, myocardial diseases, myocardial ischemia, pericardial effusion, pericarditis (including constrictive and 15 tuberculous), pneumopericardium, postpericardiotomy syndrome, pulmonary heart disease, rheumatic heart disease, ventricular dysfunction, hyperemia, cardiovascular pregnancy complications, Scimitar Syndrome, cardiovascular syphilis, and cardiovascular tuberculosis.

Arrhythmias include sinus arrhythmia, atrial fibrillation, atrial flutter, bradycardia, extrasystole, Adams-Stokes Syndrome, bundle-branch block, sinoatrial block, long QT 20 syndrome, parasytole, Lown-Ganong-Levine Syndrome, Mahaim-type pre-excitation syndrome, Wolff-Parkinson-White syndrome, sick sinus syndrome, tachycardias, and ventricular fibrillation. Tachycardias include paroxysmal tachycardia, supraventricular tachycardia, accelerated idioventricular rhythm, atrioventricular nodal reentry tachycardia, ectopic atrial tachycardia, ectopic junctional tachycardia, sinoatrial nodal reentry tachycardia, 25 sinus tachycardia, Torsades de Pointes, and ventricular tachycardia.

Heart valve disease include aortic valve insufficiency, aortic valve stenosis, hear murmurs, aortic valve prolapse, mitral valve prolapse, tricuspid valve prolapse, mitral valve insufficiency, mitral valve stenosis, pulmonary atresia, pulmonary valve insufficiency, pulmonary valve stenosis, tricuspid atresia, tricuspid valve insufficiency, and tricuspid valve 30 stenosis.

Myocardial diseases include alcoholic cardiomyopathy, congestive cardiomyopathy, hypertrophic cardiomyopathy, aortic subvalvular stenosis, pulmonary subvalvular stenosis,

restrictive cardiomyopathy, Chagas cardiomyopathy, endocardial fibroelastosis, endomyocardial fibrosis, Kearns Syndrome, myocardial reperfusion injury, and myocarditis.

Myocardial ischemias include coronary disease, such as angina pectoris, coronary aneurysm, coronary arteriosclerosis, coronary thrombosis, coronary vasospasm, myocardial infarction and myocardial stunning.

Cardiovascular diseases also include vascular diseases such as aneurysms, angiodyplasia, angiomas, bacillary angiomas, Hippel-Lindau Disease, Klippel-Trenaunay-Weber Syndrome, Sturge-Weber Syndrome, angioneurotic edema, aortic diseases, Takayasu's Arteritis, aortitis, Leriche's Syndrome, arterial occlusive diseases, arteritis, 10 enarteritis, polyarteritis nodosa, cerebrovascular disorders, diabetic angiopathies, diabetic retinopathy, embolisms, thrombosis, erythromelalgia, hemorrhoids, hepatic veno-occlusive disease, hypertension, hypotension, ischemia, peripheral vascular diseases, phlebitis, pulmonary veno-occlusive disease, Raynaud's disease, CREST syndrome, retinal vein occlusion, Scimitar syndrome, superior vena cava syndrome, telangiectasia, atacia 15 telangiectasia, hereditary hemorrhagic telangiectasia, varicocele, varicose veins, varicose ulcer, vasculitis, and venous insufficiency.

Aneurysms include dissecting aneurysms, false aneurysms, infected aneurysms, ruptured aneurysms, aortic aneurysms, cerebral aneurysms, coronary aneurysms, heart aneurysms, and iliac aneurysms.

Arterial occlusive diseases include arteriosclerosis, intermittent claudication, carotid stenosis, fibromuscular dysplasias, mesenteric vascular occlusion, Moyamoya disease, renal artery obstruction, retinal artery occlusion, and thromboangiitis obliterans.

Cerebrovascular disorders include carotid artery diseases, cerebral amyloid angiopathy, cerebral aneurysm, cerebral anoxia, cerebral arteriosclerosis, cerebral arteriovenous malformation, cerebral artery diseases, cerebral embolism and thrombosis, carotid artery thrombosis, sinus thrombosis, Wallenberg's syndrome, cerebral hemorrhage, epidural hematoma, subdural hematoma, subarachnoid hemorrhage, cerebral infarction, cerebral ischemia (including transient), subclavian steal syndrome, periventricular leukomalacia, vascular headache, cluster headache, migraine, and vertebrobasilar 30 insufficiency.

Embolisms include air embolisms, amniotic fluid embolisms, cholesterol embolisms, blue toe syndrome, fat embolisms, pulmonary embolisms, and thromboembolisms.

Thrombosis include coronary thrombosis, hepatic vein thrombosis, retinal vein occlusion, carotid artery thrombosis, sinus thrombosis, Wallenberg's syndrome, and thrombophlebitis.

Ischemia includes cerebral ischemia, ischemic colitis, compartment syndromes, anterior compartment syndrome, myocardial ischemia, reperfusion injuries, and peripheral limb ischemia. Vasculitis includes aortitis, arteritis, Behcet's Syndrome, Churg-Strauss Syndrome, mucocutaneous lymph node syndrome, thromboangiitis obliterans, hypersensitivity vasculitis, Schoenlein-Henoch purpura, allergic cutaneous vasculitis, and Wegener's granulomatosis.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention, 10 are especially effective for the treatment of critical limb ischemia and coronary disease.

Polypeptides may be administered using any method known in the art, including, but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, biostatic injectors, particle accelerators, gelfoam sponge depots, other commercially available depot materials, osmotic pumps, oral or suppositorial 15 solid pharmaceutical formulations, decanting or topical applications during surgery, aerosol delivery. Such methods are known in the art. Polypeptides may be administered as part of a Therapeutic, described in more detail below. Methods of delivering polynucleotides are described in more detail herein.

20 Anti-Angiogenesis Activity

The naturally occurring balance between endogenous stimulators and inhibitors of angiogenesis is one in which inhibitory influences predominate. Rastinejad *et al.*, *Cell* 56:345-355 (1989). In those rare instances in which neovascularization occurs under normal physiological conditions, such as wound healing, organ regeneration, embryonic 25 development, and female reproductive processes, angiogenesis is stringently regulated and spatially and temporally delimited. Under conditions of pathological angiogenesis such as that characterizing solid tumor growth, these regulatory controls fail. Unregulated angiogenesis becomes pathologic and sustains progression of many neoplastic and non-neoplastic diseases. A number of serious diseases are dominated by abnormal 30 neovascularization including solid tumor growth and metastases, arthritis, some types of eye disorders, and psoriasis. See, e.g., reviews by Moses *et al.*, *Biotech.* 9:630-634 (1991); Folkman *et al.*, *N. Engl. J. Med.*, 333:1757-1763 (1995); Auerbach *et al.*, *J. Microvasc. Res.*

29:401-411 (1985); Folkman, Advances in Cancer Research, eds. Klein and Weinhouse, Academic Press. New York, pp. 175-203 (1985); Patz, *Am. J. Ophthalmol.* 94:715-743 (1982); and Folkman *et al.*, *Science* 221:719-725 (1983). In a number of pathological conditions, the process of angiogenesis contributes to the disease state. For example, 5 significant data have accumulated which suggest that the growth of solid tumors is dependent on angiogenesis. Folkman and Klagsbrun, *Science* 235:442-447 (1987).

The polynucleotides encoding a polypeptide of the present invention may be administered along with other polynucleotides encoding an angiogenic protein. Examples of angiogenic proteins include, but are not limited to, acidic and basic fibroblast growth factors. 10 VEGF-1, VEGF-2, VEGF-3, epidermal growth factor alpha and beta, platelet-derived endothelial cell growth factor, platelet-derived growth factor, tumor necrosis factor alpha, hepatocyte growth factor, insulin like growth factor, colony stimulating factor, macrophage colony stimulating factor, granulocyte/macrophage colony stimulating factor, and nitric oxide synthase.

15 The present invention provides for treatment of diseases or disorders associated with neovascularization by administration of the polynucleotides and/or polypeptides of the invention, as well as agonists or antagonists of the present invention. Malignant and metastatic conditions which can be treated with the polynucleotides and polypeptides, or agonists or antagonists of the invention include, but are not limited to, malignancies, solid tumors, and cancers described herein and otherwise known in the art (for a review of such disorders, see Fishman *et al.*, Medicine, 2d Ed., J. B. Lippincott Co., Philadelphia 20 (1985)). Thus, the present invention provides a method of treating an angiogenesis-related disease and/or disorder, comprising administering to an individual in need thereof a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist 25 of the invention. For example, polynucleotides, polypeptides, antagonists and/or agonists may be utilized in a variety of additional methods in order to therapeutically treat a cancer or tumor. Cancers which may be treated with polynucleotides, polypeptides, antagonists and/or agonists include, but are not limited to solid tumors, including colon, rectum, prostate, lung, breast, ovarian, stomach, pancreas, larynx, esophagus, testes, liver, parotid, biliary tract, cervix, uterus, endometrium, kidney, bladder, thyroid cancer; primary tumors and metastases; 30 melanomas; glioblastoma; Kaposi's sarcoma; leiomyosarcoma; non- small cell lung cancer; colorectal cancer; advanced malignancies; and blood born tumors such as leukemias. For

example, polynucleotides, polypeptides, antagonists and/or agonists may be delivered topically, in order to treat cancers such as skin cancer, head and neck tumors, breast tumors, and Kaposi's sarcoma.

Within yet other aspects, polynucleotides, polypeptides, antagonists and/or agonists 5 may be utilized to treat superficial forms of bladder cancer by, for example, intravesical administration. Polynucleotides, polypeptides, antagonists and/or agonists may be delivered directly into the tumor, or near the tumor site, via injection or a catheter. Of course, as the artisan of ordinary skill will appreciate, the appropriate mode of administration will vary according to the cancer to be treated. Other modes of delivery are discussed herein.

10 Polynucleotides, polypeptides, antagonists and/or agonists may be useful in treating other disorders, besides cancers, which involve angiogenesis. These disorders include, but are not limited to: benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas; arteriosclerotic plaques; ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular 15 degeneration, corneal graft rejection, neovascular glaucoma, retrobulbar fibroplasia, rubeosis, retinoblastoma, uveitis and Pterygia (abnormal blood vessel growth) of the eye; rheumatoid arthritis; psoriasis; delayed wound healing; endometriosis; vasculogenesis; granulations; hypertrophic scars (keloids); nonunion fractures; scleroderma; trachoma; vascular adhesions; myocardial angiogenesis; coronary collaterals; cerebral collaterals; arteriovenous 20 malformations; ischemic limb angiogenesis; Osler-Webber Syndrome; plaque neovascularization; telangiectasia; hemophiliac joints; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; and atherosclerosis.

For example, within one aspect of the present invention methods are provided for 25 treating hypertrophic scars and keloids, comprising the step of administering a polynucleotide, polypeptide, antagonist and/or agonist of the invention to a hypertrophic scar or keloid.

Within one embodiment of the present invention polynucleotides, polypeptides, antagonists and/or agonists are directly injected into a hypertrophic scar or keloid, in order to prevent the progression of these lesions. This therapy is of particular value in the 30 prophylactic treatment of conditions which are known to result in the development of hypertrophic scars and keloids (e.g., burns), and is preferably initiated after the proliferative phase has had time to progress (approximately 14 days after the initial injury), but before

hypertrophic scar or keloid development. As noted above, the present invention also provides methods for treating neovascular diseases of the eye, including for example, corneal neovascularization, neovascular glaucoma, proliferative diabetic retinopathy, retrolental fibroplasia and macular degeneration.

- 5 Moreover, Ocular disorders associated with neovascularization which can be treated with the polynucleotides and polypeptides of the present invention (including agonists and/or antagonists) include, but are not limited to: neovascular glaucoma, diabetic retinopathy, retinoblastoma, retrolental fibroplasia, uveitis, retinopathy of prematurity macular degeneration, corneal graft neovascularization, as well as other eye inflammatory diseases,
10 ocular tumors and diseases associated with choroidal or iris neovascularization. See, e.g., reviews by Waltman *et al.*, *Am. J. Ophthal.* 85:704-710 (1978) and Gartner *et al.*, *Surv. Ophthal.* 22:291-312 (1978).

Thus, within one aspect of the present invention methods are provided for treating neovascular diseases of the eye such as corneal neovascularization (including corneal graft neovascularization), comprising the step of administering to a patient a therapeutically effective amount of a compound (as described above) to the cornea, such that the formation of blood vessels is inhibited. Briefly, the cornea is a tissue which normally lacks blood vessels. In certain pathological conditions however, capillaries may extend into the cornea from the pericorneal vascular plexus of the limbus. When the cornea becomes vascularized, it also becomes clouded, resulting in a decline in the patient's visual acuity. Visual loss may become complete if the cornea completely opacitates. A wide variety of disorders can result in corneal neovascularization, including for example, corneal infections (e.g., trachoma, herpes simplex keratitis, leishmaniasis and onchocerciasis), immunological processes (e.g., graft rejection and Stevens-Johnson's syndrome), alkali burns, trauma, inflammation (of any cause), toxic and nutritional deficiency states, and as a complication of wearing contact lenses.
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Within particularly preferred embodiments of the invention, may be prepared for topical administration in saline (combined with any of the preservatives and antimicrobial agents commonly used in ocular preparations), and administered in eyedrop form. The solution or suspension may be prepared in its pure form and administered several times daily. Alternatively, anti-angiogenic compositions, prepared as described above, may also be administered directly to the cornea. Within preferred embodiments, the anti-angiogenic
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composition is prepared with a muco-adhesive polymer which binds to cornea. Within further embodiments, the anti-angiogenic factors or anti-angiogenic compositions may be utilized as an adjunct to conventional steroid therapy. Topical therapy may also be useful prophylactically in corneal lesions which are known to have a high probability of inducing an 5 angiogenic response (such as chemical burns). In these instances the treatment, likely in combination with steroids, may be instituted immediately to help prevent subsequent complications.

Within other embodiments, the compounds described above may be injected directly 10 into the corneal stroma by an ophthalmologist under microscopic guidance. The preferred site of injection may vary with the morphology of the individual lesion, but the goal of the administration would be to place the composition at the advancing front of the vasculature (i.e., interspersed between the blood vessels and the normal cornea). In most cases this would involve perlimbic corneal injection to "protect" the cornea from the advancing blood vessels. This method may also be utilized shortly after a corneal insult in order to 15 prophylactically prevent corneal neovascularization. In this situation the material could be injected in the perlimbic cornea interspersed between the corneal lesion and its undesired potential limbic blood supply. Such methods may also be utilized in a similar fashion to prevent capillary invasion of transplanted corneas. In a sustained-release form injections might only be required 2-3 times per year. A steroid could also be added to the injection 20 solution to reduce inflammation resulting from the injection itself.

Within another aspect of the present invention, methods are provided for treating neovascular glaucoma, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eye, such that the formation of blood vessels is inhibited. In one embodiment, the compound may be 25 administered topically to the eye in order to treat early forms of neovascular glaucoma. Within other embodiments, the compound may be implanted by injection into the region of the anterior chamber angle. Within other embodiments, the compound may also be placed in any location such that the compound is continuously released into the aqueous humor. Within another aspect of the present invention, methods are provided for treating 30 proliferative diabetic retinopathy, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eyes, such that the formation of blood vessels is inhibited.

Within particularly preferred embodiments of the invention, proliferative diabetic retinopathy may be treated by injection into the aqueous humor or the vitreous, in order to increase the local concentration of the polynucleotide, polypeptide, antagonist and/or agonist in the retina. Preferably, this treatment should be initiated prior to the acquisition of severe disease requiring photocoagulation.

Within another aspect of the present invention, methods are provided for treating retrobulbar fibroplasia, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eye, such that the formation of blood vessels is inhibited. The compound may be administered topically, via intravitreous injection and/or via intraocular implants.

Additionally, disorders which can be treated with the polynucleotides, polypeptides, agonists and/or agonists include, but are not limited to, hemangioma, arthritis, psoriasis, angiomyoma, atherosclerotic plaques, delayed wound healing, granulations, hemophilic joints, hypertrophic scars, nonunion fractures, Osler-Weber syndrome, pyogenic granuloma, scleroderma, trachoma, and vascular adhesions.

Moreover, disorders and/or states, which can be treated with the polynucleotides, polypeptides, agonists and/or agonists include, but are not limited to, solid tumors, blood born tumors such as leukemias, tumor metastasis, Kaposi's sarcoma, benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrobulbar fibroplasia, rubeosis, retinoblastoma, and uveitis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars (keloids), nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, Osler-Webber Syndrome, plaque neovascularization, telangiectasia, hemophiliac joints, angiomyoma fibromuscular dysplasia, wound granulation, Crohn's disease, atherosclerosis, birth control agent by preventing vascularization required for embryo implantation controlling menstruation, diseases that have angiogenesis as a pathologic consequence such as cat scratch disease (Rochelle minalia quintosa), ulcers (*Helicobacter pylori*), Bartonellosis and bacillary angiomatosis.

In one aspect of the birth control method, an amount of the compound sufficient to block embryo implantation is administered before or after intercourse and fertilization have occurred, thus providing an effective method of birth control, possibly a "morning after" method. Polynucleotides, polypeptides, agonists and/or agonists may also be used in controlling menstruation or administered as either a peritoneal lavage fluid or for peritoneal implantation in the treatment of endometriosis.

Polynucleotides, polypeptides, agonists and/or agonists of the present invention may be incorporated into surgical sutures in order to prevent stitch granulomas.

Polynucleotides, polypeptides, agonists and/or agonists may be utilized in a wide variety of surgical procedures. For example, within one aspect of the present invention a compositions (in the form of, for example, a spray or film) may be utilized to coat or spray an area prior to removal of a tumor, in order to isolate normal surrounding tissues from malignant tissue, and/or to prevent the spread of disease to surrounding tissues. Within other aspects of the present invention, compositions (e.g., in the form of a spray) may be delivered via endoscopic procedures in order to coat tumors, or inhibit angiogenesis in a desired locale. Within yet other aspects of the present invention, surgical meshes which have been coated with anti-angiogenic compositions of the present invention may be utilized in any procedure wherein a surgical mesh might be utilized. For example, within one embodiment of the invention a surgical mesh laden with an anti-angiogenic composition may be utilized during abdominal cancer resection surgery (e.g., subsequent to colon resection) in order to provide support to the structure, and to release an amount of the anti-angiogenic factor.

Within further aspects of the present invention, methods are provided for treating tumor excision sites, comprising administering a polynucleotide, polypeptide, agonist and/or agonist to the resection margins of a tumor subsequent to excision, such that the local recurrence of cancer and the formation of new blood vessels at the site is inhibited. Within one embodiment of the invention, the anti-angiogenic compound is administered directly to the tumor excision site (e.g., applied by swabbing, brushing or otherwise coating the resection margins of the tumor with the anti-angiogenic compound). Alternatively, the anti-angiogenic compounds may be incorporated into known surgical pastes prior to administration. Within particularly preferred embodiments of the invention, the anti-angiogenic compounds are applied after hepatic resections for malignancy, and after neurosurgical operations.

Within one aspect of the present invention, polynucleotides, polypeptides, agonists and/or agonists may be administered to the resection margin of a wide variety of tumors, including for example, breast, colon, brain and hepatic tumors. For example, within one embodiment of the invention, anti-angiogenic compounds may be administered to the site of 5 a neurological tumor subsequent to excision, such that the formation of new blood vessels at the site are inhibited.

The polynucleotides, polypeptides, agonists and/or agonists of the present invention may also be administered along with other anti-angiogenic factors. Representative examples of other anti-angiogenic factors include: Anti-Invasive Factor, retinoic acid and derivatives 10 thereof, paclitaxel, Suramin, Tissue Inhibitor of Metalloproteinase-1, Tissue Inhibitor of Metalloproteinase-2, Plasminogen Activator Inhibitor-1, Plasminogen Activator Inhibitor-2, and various forms of the lighter "d group" transition metals.

Lighter "d group" transition metals include, for example, vanadium, molybdenum, tungsten, titanium, niobium, and tantalum species. Such transition metal species may form 15 transition metal complexes. Suitable complexes of the above-mentioned transition metal species include oxo transition metal complexes.

Representative examples of vanadium complexes include oxo vanadium complexes such as vanadate and vanadyl complexes. Suitable vanadate complexes include metavanadate and orthovanadate complexes such as, for example, ammonium metavanadate, 20 sodium metavanadate, and sodium orthovanadate. Suitable vanadyl complexes include, for example, vanadyl acetylacetone and vanadyl sulfate including vanadyl sulfate hydrates such as vanadyl sulfate mono- and trihydrates.

Representative examples of tungsten and molybdenum complexes also include oxo complexes. Suitable oxo tungsten complexes include tungstate and tungsten oxide 25 complexes. Suitable tungstate complexes include ammonium tungstate, calcium tungstate, sodium tungstate dihydrate, and tungstic acid. Suitable tungsten oxides include tungsten (IV) oxide and tungsten (VI) oxide. Suitable oxo molybdenum complexes include molybdate, molybdenum oxide, and molybdenyl complexes. Suitable molybdate complexes include ammonium molybdate and its hydrates, sodium molybdate and its hydrates, and potassium 30 molybdate and its hydrates. Suitable molybdenum oxides include molybdenum (VI) oxide, molybdenum (VI) oxide, and molybdic acid. Suitable molybdenyl complexes include, for

example, molybdenyl acetylacetone. Other suitable tungsten and molybdenum complexes include hydroxo derivatives derived from, for example, glycerol, tartaric acid, and sugars.

A wide variety of other anti-angiogenic factors may also be utilized within the context of the present invention. Representative examples include platelet factor 4; protamine sulphate; sulphated chitin derivatives (prepared from queen crab shells), (Murata et al., Cancer Res. 51:22-26, 1991); Sulphated Polysaccharide Peptidoglycan Complex (SP-PG) (the function of this compound may be enhanced by the presence of steroids such as estrogen, and tamoxifen citrate); Staurosporine; modulators of matrix metabolism, including for example, proline analogs, cishydroxyproline, d,L-3,4-dehydroproline, Thiaproline, alpha,alpha-dipyridyl, aminopropionitrile fumarate; 4-propyl-5-(4-pyridinyl)-2(3H)-oxazolone; Methotrexate; Mitoxantrone; Heparin; Interferons; 2 Macroglobulin-serum; ChIMP-3 (Pavloff et al., J. Bio. Chem. 267:17321-17326, 1992); Chymostatin (Tomkinson et al., Biochem J. 286:475-480, 1992); Cyclodextrin Tetradecasulfate; Eponemycin; Camptothecin; Fumagillin (Ingber et al., Nature 348:555-557, 1990); Gold Sodium Thiomalate ("GST"; Matsubara and Ziff, J. Clin. Invest. 79:1440-1446, 1987); anticollagenase-serum; alpha2-antiplasmin (Holmes et al., J. Biol. Chem. 262(4):1659-1664, 1987); Bisantrene (National Cancer Institute); Lobenzarit disodium (N-(2)-carboxyphenyl-4-chloroanthronilic acid disodium or "CCA"; Takeuchi et al., Agents Actions 36:312-316, 1992); Thalidomide; Angostatic steroid; AGM-1470; carboxynaminolmidazole; and metalloproteinase inhibitors such as BB94.

Diseases at the Cellular Level

Diseases associated with increased cell survival or the inhibition of apoptosis that could be treated or detected by polynucleotides or polypeptides, as well as antagonists or agonists of the present invention, include cancers (such as follicular lymphomas, carcinomas with p53 mutations, and hormone-dependent tumors, including, but not limited to colon cancer, cardiac tumors, pancreatic cancer, melanoma, retinoblastoma, glioblastoma, lung cancer, intestinal cancer, testicular cancer, stomach cancer, neuroblastoma, myxoma, myoma, lymphoma, endothelioma, osteoblastoma, osteoclastoma, osteosarcoma, chondrosarcoma, adenoma, breast cancer, prostate cancer, Kaposi's sarcoma and ovarian cancer); autoimmune disorders (such as, multiple sclerosis, Sjogren's syndrome, Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and

immune-related glomerulonephritis and rheumatoid arthritis) and viral infections (such as herpes viruses, pox viruses and adenoviruses), inflammation, graft v. host disease, acute graft rejection, and chronic graft rejection. In preferred embodiments, polynucleotides, polypeptides, and/or antagonists of the invention are used to inhibit growth, progression, and/or metastasis of cancers, in particular those listed above.

Additional diseases or conditions associated with increased cell survival that could be treated or detected by polynucleotides or polypeptides, or agonists or antagonists of the present invention include, but are not limited to, progression, and/or metastases of malignancies and related disorders such as leukemia (including acute leukemias (e.g., acute lymphocytic leukemia, acute myelocytic leukemia (including myeloblastic, promyelocytic, myelomonocytic, monocytic, and erythroleukemia)) and chronic leukemias (e.g., chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia)), polycythemia vera, lymphomas (e.g., Hodgkin's disease and non-Hodgkin's disease), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, and solid tumors including, but not limited to, sarcomas and carcinomas such as fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endothelirosarcoma, lymphangiosarcoma, lymphangioendothelirosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical cancer, testicular tumor, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendrogioma, menangioma, melanoma, neuroblastoma, and retinoblastoma.

Diseases associated with increased apoptosis that could be treated or detected by polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, include AIDS; neurodegenerative disorders (such as Alzheimer's disease, Parkinson's disease, Amyotrophic lateral sclerosis, Retinitis pigmentosa, Cerebellar degeneration and brain tumor or prior associated disease); autoimmune disorders (such as, multiple sclerosis, Sjogren's

syndrome. Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and immune-related glomerulonephritis and rheumatoid arthritis) myelodysplastic syndromes (such as aplastic anemia), graft v. host disease, ischemic injury (such as that caused by myocardial infarction, stroke and reperfusion 5 injury), liver injury (e.g., hepatitis related liver injury, ischemia/reperfusion injury, cholestasis (bile duct injury) and liver cancer); toxin-induced liver disease (such as that caused by alcohol); septic shock, cachexia and anorexia.

Wound Healing and Epithelial Cell Proliferation

10 In accordance with yet a further aspect of the present invention, there is provided a process for utilizing polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, for therapeutic purposes, for example, to stimulate epithelial cell proliferation and basal keratinocytes for the purpose of wound healing, and to stimulate hair follicle production and healing of dermal wounds. Polynucleotides or polypeptides, as well as 15 agonists or antagonists of the present invention, may be clinically useful in stimulating wound healing including surgical wounds, excisional wounds, deep wounds involving damage of the dermis and epidermis, eye tissue wounds, dental tissue wounds, oral cavity wounds, diabetic ulcers, dermal ulcers, cubitus ulcers, arterial ulcers, venous stasis ulcers, burns resulting from heat exposure or chemicals, and other abnormal wound healing 20 conditions such as uremia, malnutrition, vitamin deficiencies and complications associated with systemic treatment with steroids, radiation therapy and antineoplastic drugs and antimetabolites. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to promote dermal reestablishment subsequent to dermal loss

25 Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to increase the adherence of skin grafts to a wound bed and to stimulate re-epithelialization from the wound bed. The following are types of grafts that 30 polynucleotides or polypeptides, agonists or antagonists of the present invention, could be used to increase adherence to a wound bed: autografts, artificial skin, allografts, autodermic graft, autoepidermic grafts, avascular grafts, Blair-Brown grafts, bone graft, brepheplastic grafts, cutis graft, delayed graft, dermic graft, epidermic graft, fascia graft, full thickness graft, heterologous graft, xenograft, homologous graft, hyperplastic graft, lamellar graft,

mesh graft, mucosal graft, Ollier-Thiersch graft, omenpal graft, patch graft, pedicle graft, penetrating graft, split skin graft, thick split graft. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, can be used to promote skin strength and to improve the appearance of aged skin.

5 It is believed that polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, will also produce changes in hepatocyte proliferation, and epithelial cell proliferation in the lung, breast, pancreas, stomach, small intestine, and large intestine. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could promote proliferation of epithelial cells such as sebocytes, hair follicles, hepatocytes, 10 type II pneumocytes, mucin-producing goblet cells, and other epithelial cells and their progenitors contained within the skin, lung, liver, and gastrointestinal tract. Polynucleotides or polypeptides, agonists or antagonists of the present invention, may promote proliferation of endothelial cells, keratinocytes, and basal keratinocytes.

15 Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could also be used to reduce the side effects of gut toxicity that result from radiation, chemotherapy treatments or viral infections. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, may have a cytoprotective effect on the small intestine mucosa. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, may also stimulate healing of mucositis (mouth ulcers) 20 that result from chemotherapy and viral infections.

25 Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could further be used in full regeneration of skin in full and partial thickness skin defects, including burns, (i.e., repopulation of hair follicles, sweat glands, and sebaceous glands), treatment of other skin defects such as psoriasis. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to treat epidermolysis bullosa, a defect in adherence of the epidermis to the underlying dermis which results in frequent, open and painful blisters by accelerating reepithelialization of these lesions. 30 Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could also be used to treat gastric and duodenal ulcers and help heal by scar formation of the mucosal lining and regeneration of glandular mucosa and duodenal mucosal lining more rapidly. Inflammatory bowel diseases, such as Crohn's disease and ulcerative colitis, are diseases which result in destruction of the mucosal surface of the small or large intestine,

- respectively. Thus, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to promote the resurfacing of the mucosal surface to aid more rapid healing and to prevent progression of inflammatory bowel disease. Treatment with polynucleotides or polypeptides, agonists or antagonists of the present invention, is 5 expected to have a significant effect on the production of mucus throughout the gastrointestinal tract and could be used to protect the intestinal mucosa from injurious substances that are ingested or following surgery. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to treat diseases associate with the under expression.
- 10 Moreover, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to prevent and heal damage to the lungs due to various pathological states. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, which could stimulate proliferation and differentiation and promote the repair of alveoli and bronchiolar epithelium to prevent or treat acute or chronic lung damage.
- 15 For example, emphysema, which results in the progressive loss of aveoli, and inhalation injuries, i.e., resulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli could be effectively treated using polynucleotides or polypeptides, agonists or antagonists of the present invention. Also, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to stimulate the 20 proliferation of and differentiation of type II pneumocytes, which may help treat or prevent disease such as hyaline membrane diseases, such as infant respiratory distress syndrome and bronchopulmonary displasia, in premature infants.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could stimulate the proliferation and differentiation of hepatocytes and, thus, could 25 be used to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances (i.e., acetaminophen, carbon tetrachloride and other hepatotoxins known in the art).

In addition, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used treat or prevent the onset of diabetes mellitus. In patients 30 with newly diagnosed Types I and II diabetes, where some islet cell function remains, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to maintain the islet function so as to alleviate, delay or prevent permanent

manifestation of the disease. Also, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used as an auxiliary in islet cell transplantation to improve or promote islet cell function.

5 Neurological Diseases

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, for therapeutic purposes, for example, to stimulate neurological cell proliferation and/or differentiation. Therefore, polynucleotides, polypeptides, agonists and/or antagonists of the invention may be used to treat and/or detect neurologic diseases. Moreover, polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used as a marker or detector of a particular nervous system disease or disorder.

Examples of neurologic diseases which can be treated or detected with polynucleotides, polypeptides, agonists, and/or antagonists of the present invention include brain diseases, such as metabolic brain diseases which includes phenylketonuria such as maternal phenylketonuria, pyruvate carboxylase deficiency, pyruvate dehydrogenase complex deficiency, Wernicke's Encephalopathy, brain edema, brain neoplasms such as cerebellar neoplasms which include infratentorial neoplasms, cerebral ventricle neoplasms such as choroid plexus neoplasms, hypothalamic neoplasms, supratentorial neoplasms, canavan disease, cerebellar diseases such as cerebellar ataxia which include spinocerebellar degeneration such as ataxia telangiectasia, cerebellar dyssynergia, Friederich's Ataxia, Machado-Joseph Disease, olivopontocerebellar atrophy, cerebellar neoplasms such as infratentorial neoplasms, diffuse cerebral sclerosis such as encephalitis periaxialis, globoid cell leukodystrophy, metachromatic leukodystrophy and subacute sclerosing panencephalitis, cerebrovascular disorders (such as carotid artery diseases which include carotid artery thrombosis, carotid stenosis and Moyamoya Disease, cerebral amyloid angiopathy, cerebral aneurysm, cerebral anoxia, cerebral arteriosclerosis, cerebral arteriovenous malformations, cerebral artery diseases, cerebral embolism and thrombosis such as carotid artery thrombosis, sinus thrombosis and Wallenberg's Syndrome, cerebral hemorrhage such as epidural hematoma, subdural hematoma and subarachnoid hemorrhage, cerebral infarction, cerebral ischemia such as transient cerebral ischemia, Subclavian Steal Syndrome and vertebrobasilar insufficiency, vascular dementia such as multi-infarct dementia, periventricular leukomalacia,

vascular headache such as cluster headache, migraine, dementia such as AIDS Dementia Complex, presenile dementia such as Alzheimer's Disease and Creutzfeldt-Jakob Syndrome, senile dementia such as Alzheimer's Disease and progressive supranuclear palsy, vascular dementia such as multi-infarct dementia, encephalitis which include encephalitis periaxialis, 5 viral encephalitis such as epidemic encephalitis, Japanese Encephalitis, St. Louis Encephalitis, tick-borne encephalitis and West Nile Fever, acute disseminated encephalomyelitis, meningoencephalitis such as uveomeningoencephalitic syndrome, Postencephalitic Parkinson Disease and subacute sclerosing panencephalitis, encephalomalacia such as periventricular leukomalacia, epilepsy such as generalized epilepsy 10 which includes infantile spasms, absence epilepsy, myoclonic epilepsy which includes MERRF Syndrome, tonic-clonic epilepsy, partial epilepsy such as complex partial epilepsy, frontal lobe epilepsy and temporal lobe epilepsy, post-traumatic epilepsy, status epilepticus such as Epilepsia Partialis Continua, Hallervorden-Spatz Syndrome, hydrocephalus such as Dandy-Walker Syndrome and normal pressure hydrocephalus, hypothalamic diseases such as 15 hypothalamic neoplasms, cerebral malaria, narcolepsy which includes cataplexy, bulbar poliomyelitis, cerebri pseudotumor, Rett Syndrome, Reye's Syndrome, thalamic diseases, cerebral toxoplasmosis, intracranial tuberculoma and Zellweger Syndrome, central nervous system infections such as AIDS Dementia Complex, Brain Abscess, subdural empyema, encephalomyelitis such as Equine Encephalomyelitis, Venezuelan Equine Encephalomyelitis, 20 Necrotizing Hemorrhagic Encephalomyelitis, Visna, cerebral malaria, meningitis such as arachnoiditis, aseptic meningitis such as viral meningitis which includes lymphocytic choriomeningitis. Bacterial meningitis which includes Haemophilus Meningitis, Listeria Meningitis. Meningococcal Meningitis such as Waterhouse-Friderichsen Syndrome, Pneumococcal Meningitis and meningeal tuberculosis, fungal meningitis such as 25 Cryptococcal Meningitis, subdural effusion, meningoencephalitis such as uveomeningoencephalitic syndrome, myelitis such as transverse myelitis, neurosyphilis such as tabes dorsalis, poliomyelitis which includes bulbar poliomyelitis and postpoliomyelitis syndrome, prion diseases (such as Creutzfeldt-Jakob Syndrome, Bovine Spongiform Encephalopathy, Gerstmann-Straussler Syndrome, Kuru, Scrapie) cerebral toxoplasmosis, 30 central nervous system neoplasms such as brain neoplasms that include cerebellar neoplasms such as infratentorial neoplasms, cerebral ventricle neoplasms such as choroid plexus neoplasms, hypothalamic neoplasms and supratentorial neoplasms, meningeal

neoplasms, spinal cord neoplasms which include epidural neoplasms, demyelinating diseases such as Canavan Diseases, diffuse cerebral sceloris which includes adrenoleukodystrophy, encephalitis periaxialis, globoid cell leukodystrophy, diffuse cerebral sclerosis such as metachromatic leukodystrophy, allergic encephalomyelitis, necrotizing hemorrhagic encephalomyelitis, progressive multifocal leukoencephalopathy, multiple sclerosis, central pontine myelinolysis, transverse myelitis, neuromyelitis optica, Scrapie, Swayback, Chronic Fatigue Syndrome, Visna, High Pressure Nervous Syndrome, Meningism, spinal cord diseases such as amyotonia congenita, amyotrophic lateral sclerosis, spinal muscular atrophy such as Werdnig-Hoffmann Disease, spinal cord compression, spinal cord neoplasms such as 5 epidural neoplasms, syringomyelia, Tabes Dorsalis, Stiff-Man Syndrome, mental retardation such as Angelman Syndrome, Cri-du-Chat Syndrome, De Lange's Syndrome, Down Syndrome, Gangliosidoses such as gangliosidoses G(M1), Sandhoff Disease, Tay-Sachs Disease, Hartnup Disease, homocystinuria, Laurence-Moon- Biedl Syndrome, Lesch-Nyhan Syndrome, Maple Syrup Urine Disease, mucolipidosis such as fucosidosis, neuronal ceroid- 10 lipofuscinosis, oculocerebrorenal syndrome, phenylketonuria such as maternal phenylketonuria, Prader-Willi Syndrome, Rett Syndrome, Rubinstein-Taybi Syndrome, Tuberous Sclerosis, WAGR Syndrome, nervous system abnormalities such as holoprosencephaly, neural tube defects such as anencephaly which includes hydranencephaly, Arnold-Chairi Deformity, encephalocele, meningocele, 15 meningomyelocele, spinal dysraphism such as spina bifida cystica and spina bifida occulta, hereditary motor and sensory neuropathies which include Charcot-Marie Disease, Hereditary optic atrophy, Refsum's Disease, hereditary spastic paraplegia, Werdnig-Hoffmann Disease, Hereditary Sensory and Autonomic Neuropathies such as Congenital Analgesia and Familial Dysautonomia, Neurologic manifestations (such as agnosia that include Gerstmann's 20 Syndrome, Amnesia such as retrograde amnesia, apraxia, neurogenic bladder, cataplexy, communicative disorders such as hearing disorders that includes deafness, partial hearing loss, loudness recruitment and tinnitus, language disorders such as aphasia which include agraphia, anomia, broca aphasia, and Wernicke Aphasia, Dyslexia such as Acquired Dyslexia, language development disorders, speech disorders such as aphasia which includes 25 anomia, broca aphasia and Wernicke Aphasia. articulation disorders, communicative disorders such as speech disorders which include dysarthria, echolalia, mutism and stuttering, voice disorders such as aphonia and hoarseness, decerebrate state, delirium, fasciculation, 30

hallucinations, meningism, movement disorders such as angelman syndrome, ataxia, athetosis, chorea, dystonia, hypokinesia, muscle hypotonia, myoclonus, tic, torticollis and tremor, muscle hypertonia such as muscle rigidity such as stiff-man syndrome, muscle spasticity, paralysis such as facial paralysis which includes Herpes Zoster Oticus,

5 Gastroparesis, Hemiplegia, ophthalmoplegia such as diplopia, Duane's Syndrome, Horner's Syndrome, Chronic progressive external ophthalmoplegia such as Kearns Syndrome, Bulbar Paralysis, Tropical Spastic Paraparesis, Paraplegia such as Brown-Sequard Syndrome, quadriplegia, respiratory paralysis and vocal cord paralysis, paresis, phantom limb, taste disorders such as ageusia and dysgeusia, vision disorders such as amblyopia, blindness, color

10 vision defects, diplopia, hemianopsia, scotoma and subnormal vision, sleep disorders such as hypersomnia which includes Kleine-Levin Syndrome, insomnia, and somnambulism, spasm such as trismus, unconsciousness such as coma, persistent vegetative state and syncope and vertigo, neuromuscular diseases such as amyotonia congenita, amyotrophic lateral sclerosis, Lambert-Eaton Myasthenic Syndrome, motor neuron disease, muscular atrophy such as

15 spinal muscular atrophy, Charcot-Marie Disease and Werdnig-Hoffmann Disease, Postpoliomyelitis Syndrome, Muscular Dystrophy, Myasthenia Gravis, Myotonia Atrophica, Myotonia Confinata, Nemaline Myopathy, Familial Periodic Paralysis, Multiplex Paramyoclonus, Tropical Spastic Paraparesis and Stiff-Man Syndrome, peripheral nervous system diseases such as acrodynia, amyloid neuropathies, autonomic nervous system diseases

20 such as Adie's Syndrome, Barre-Lieou Syndrome, Familial Dysautonomia, Horner's Syndrome, Reflex Sympathetic Dystrophy and Shy-Drager Syndrome, Cranial Nerve Diseases such as Acoustic Nerve Diseases such as Acoustic Neuroma which includes Neurofibromatosis 2, Facial Nerve Diseases such as Facial Neuralgia, Melkersson-Rosenthal Syndrome, ocular motility disorders which includes amblyopia, nystagmus, oculomotor nerve

25 paralysis, ophthalmoplegia such as Duane's Syndrome, Horner's Syndrome, Chronic Progressive External Ophthalmoplegia which includes Kearns Syndrome, Strabismus such as Esotropia and Exotropia, Oculomotor Nerve Paralysis, Optic Nerve Diseases such as Optic Atrophy which includes Hereditary Optic Atrophy, Optic Disk Drusen, Optic Neuritis such as Neuromyelitis Optica, Papilledema, Trigeminal Neuralgia, Vocal Cord Paralysis,

30 Demyelinating Diseases such as Neuromyelitis Optica and Swayback, Diabetic neuropathies such as diabetic foot, nerve compression syndromes such as carpal tunnel syndrome, tarsal tunnel syndrome, thoracic outlet syndrome such as cervical rib syndrome, ulnar nerve

- compression syndrome, neuralgia such as causalgia, cervico-brachial neuralgia, facial neuralgia and trigeminal neuralgia, neuritis such as experimental allergic neuritis, optic neuritis, polyneuritis, polyradiculoneuritis and radiculities such as polyradiculitis, hereditary motor and sensory neuropathies such as Charcot-Marie Disease, Hereditary Optic Atrophy, 5 Refsum's Disease, Hereditary Spastic Paraplegia and Werdnig-Hoffmann Disease, Hereditary Sensory and Autonomic Neuropathies which include Congenital Analgesia and Familial Dysautonomia, POEMS Syndrome, Sciatica, Gustatory Sweating and Tetany).

Infectious Disease

- 10 Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response.
- 15 Alternatively, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide and/or agonist or antagonist 20 of the present invention. Examples of viruses, include, but are not limited to Examples of viruses, include, but are not limited to the following DNA and RNA viruses and viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Dengue, EBV, HIV, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), 25 Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza A, Influenza B, and parainfluenza), Papiloma virus, Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, 30 but not limited to: arthritis, bronchiolitis, respiratory syncytial virus, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), Japanese B encephalitis, Junin, Chikungunya, Rift Valley fever,

yellow fever, meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases. In specific embodiments, polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat: meningitis, Dengue, EBV, and/or hepatitis (e.g., hepatitis B). In an additional specific embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat patients nonresponsive to one or more other commercially available hepatitis vaccines. In a further specific embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat AIDS.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention include, but not limited to, include, but not limited to, the following Gram-negative and Gram-positive bacteria and bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Nocardia), Cryptococcus neoformans, Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia (e.g., Borrelia burgdorferi, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, E. coli (e.g., Enterotoxigenic E. coli and Enterohemorrhagic E. coli), Enterobacteriaceae (Klebsiella, Salmonella (e.g., Salmonella typhi, and Salmonella paratyphi), Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Mycobacterium leprae, Vibrio cholerae, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Menigococcal), Meisseria meningitidis, Pasteurellacea Infections (e.g., Actinobacillus, Haemophilus (e.g., Haemophilus influenza type B), Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, Shigella spp., Staphylococcal, Meningiococcal, Pneumococcal and Streptococcal (e.g., Streptococcus pneumoniae and Group B Streptococcus). These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid,

pneumonia, Gonorrhea, meningitis (e.g., meningitis types A and B), Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections.

5 Polynucleotides or polypeptides, agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases. In specific embodiments, polynucleotides, polypeptides, agonists or antagonists of the invention are used to treat: tetanus, Diphtheria, botulism, and/or meningitis type B.

Moreover, parasitic agents causing disease or symptoms that can be treated or
10 detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention include, but not limited to, the following families or class: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas and Sporozoans (e.g., Plasmodium vivax, Plasmodium falciparum, Plasmodium
15 malariae and Plasmodium ovale). These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), malaria, pregnancy complications, and toxoplasmosis. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat or detect any of
20 these symptoms or diseases.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration
30 of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns,

incisions, or ulcers). age, disease (e.g. osteoporosis, osteoarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., 5 pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vasculature (including vascular and lymphatics), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, polynucleotides or polypeptides, as well as agonists or antagonists of the 10 present invention, may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. 15 A further example of tissue regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and 20 peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotides or 25 polypeptides, as well as agonists or antagonists of the present invention.

Chemotaxis

Polynucleotides or polypeptides, as well as agonists or antagonists of the present 30 invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of

hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules 5 can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

10 It is also contemplated that polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention could be used as an inhibitor of chemotaxis.

15 **Binding Activity**

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules 20 include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide 25 binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

30 Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

5 Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

10 Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

15 Additionally, the receptor to which the polypeptide of the present invention binds can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting (Coligan, et al., Current Protocols in Immun., 1(2), Chapter 5, (1991)). For example, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the polypeptides, for example, NIH3T3 cells which are known to contain multiple receptors for the FGF family proteins, and SC-3 cells, and a cDNA 20 library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the polypeptides. Transfected cells which are grown on glass slides are exposed to the polypeptide of the present invention, after they have been labelled. The polypeptides can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase.

25 Following fixation and incubation, the slides are subjected to auto-radiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an iterative sub-pooling and re-screening process, eventually yielding a single clones that encodes the putative receptor.

As an alternative approach for receptor identification, the labeled polypeptides can be 30 photoaffinity linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE analysis and exposed to X-ray film. The labeled complex containing the receptors of the polypeptides can be excised, resolved

into peptide fragments, and subjected to protein microsequencing. The amino acid sequence obtained from microsequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the genes encoding the putative receptors.

Moreover, the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling") may be employed to modulate the activities of the polypeptide of the present invention thereby effectively generating agonists and antagonists of the polypeptide of the present invention. See generally, U.S. Patent Nos. 5,605,793, 5,811,238, 5,830,721, 5,834,252, and 5,837,458, and Patten, P. A., et al., *Curr. Opinion Biotechnol.* 8:724-33 (1997); Harayama, S. *Trends Biotechnol.* 16(2):76-82 (1998); Hansson, L. O., et al., *J. Mol. Biol.* 287:265-76 (1999); and Lorenzo, M. M. and Blasco, R. *Biotechniques* 24(2):308-13 (1998) (each of these patents and publications are hereby incorporated by reference). In one embodiment, alteration of polynucleotides and corresponding polypeptides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments into a desired molecule by homologous, or site-specific, recombination. In another embodiment, polynucleotides and corresponding polypeptides may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of the polypeptide of the present invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules. In preferred embodiments, the heterologous molecules are family members. In further preferred embodiments, the heterologous molecule is a growth factor such as, for example, platelet-derived growth factor (PDGF), insulin-like growth factor (IGF-I), transforming growth factor (TGF)-alpha, epidermal growth factor (EGF), fibroblast growth factor (FGF), TGF-beta, bone morphogenetic protein (BMP)-2, BMP-4, BMP-5, BMP-6, BMP-7, activins A and B, decapentaplegic(dpp), 60A, OP-2, dorsalin, growth differentiation factors (GDFs), nodal, MIS, inhibin-alpha, TGF-beta1, TGF-beta2, TGF-beta3, TGF-beta5, and glial-derived neurotrophic factor (GDNF).

Other preferred fragments are biologically active fragments of the polypeptide of the present invention. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The

biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Additionally, this invention provides a method of screening compounds to identify those which modulate the action of the polypeptide of the present invention. An example of such an assay comprises combining a mammalian fibroblast cell, a the polypeptide of the present invention, the compound to be screened and ^3H thymidine under cell culture conditions where the fibroblast cell would normally proliferate. A control assay may be performed in the absence of the compound to be screened and compared to the amount of fibroblast proliferation in the presence of the compound to determine if the compound stimulates proliferation by determining the uptake of ^3H thymidine in each case. The amount of fibroblast cell proliferation is measured by liquid scintillation chromatography which measures the incorporation of ^3H thymidine. Both agonist and antagonist compounds may be identified by this procedure.

In another method, a mammalian cell or membrane preparation expressing a receptor for a polypeptide of the present invention is incubated with a labeled polypeptide of the present invention in the presence of the compound. The ability of the compound to enhance or block this interaction could then be measured. Alternatively, the response of a known second messenger system following interaction of a compound to be screened and the receptor is measured and the ability of the compound to bind to the receptor and elicit a second messenger response is measured to determine if the compound is a potential agonist or antagonist. Such second messenger systems include but are not limited to, cAMP guanylate cyclase, ion channels or phosphoinositide hydrolysis.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptides of the invention from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the present invention; and (b) determining if binding has

occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the present invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

5

Targeted Delivery

In another embodiment, the invention provides a method of delivering compositions to targeted cells expressing a receptor for a polypeptide of the invention, or cells expressing a cell bound form of a polypeptide of the invention.

10 As discussed herein, polypeptides or antibodies of the invention may be associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions. In one embodiment, the invention provides a method for the specific delivery of compositions of the invention to cells by administering polypeptides of the invention (including antibodies) that are associated with
15 heterologous polypeptides or nucleic acids. In one example, the invention provides a method for delivering a therapeutic protein into the targeted cell. In another example, the invention provides a method for delivering a single stranded nucleic acid (e.g., antisense or ribozymes) or double stranded nucleic acid (e.g., DNA that can integrate into the cell's genome or replicate episomally and that can be transcribed) into the targeted cell.

20 In another embodiment, the invention provides a method for the specific destruction of cells (e.g., the destruction of tumor cells) by administering polypeptides of the invention (e.g., polypeptides of the invention or antibodies of the invention) in association with toxins or cytotoxic prodrugs.

By "toxin" is meant compounds that bind and activate endogenous cytotoxic effector
25 systems, radioisotopes, holotoxins, modified toxins, catalytic subunits of toxins, or any molecules or enzymes not normally present in or on the surface of a cell that under defined conditions cause the cell's death. Toxins that may be used according to the methods of the invention include, but are not limited to, radioisotopes known in the art, compounds such as, for example, antibodies (or complement fixing containing portions thereof) that bind an
30 inherent or induced endogenous cytotoxic effector system, thymidine kinase, endonuclease, RNase, alpha toxin, ricin, abrin, *Pseudomonas* exotoxin A, diphtheria toxin, saporin,

momordin, gelonin, pokeweed antiviral protein, alpha-sarcin and cholera toxin. By "cytotoxic prodrug" is meant a non-toxic compound that is converted by an enzyme, normally present in the cell, into a cytotoxic compound. Cytotoxic prodrugs that may be used according to the methods of the invention include, but are not limited to, glutamyl derivatives of benzoic acid mustard alkylating agent, phosphate derivatives of etoposide or mitomycin C, cytosine arabinoside, daunorubisin, and phenoxyacetamide derivatives of doxorubicin.

Drug Screening

10 Further contemplated is the use of the polypeptides of the present invention, or the polynucleotides encoding these polypeptides, to screen for molecules which modify the activities of the polypeptides of the present invention. Such a method would include contacting the polypeptide of the present invention with a selected compound(s) suspected of having antagonist or agonist activity, and assaying the activity of these polypeptides 15 following binding.

This invention is particularly useful for screening therapeutic compounds by using the polypeptides of the present invention, or binding fragments thereof, in any of a variety of drug screening techniques. The polypeptide or fragment employed in such a test may be affixed to a solid support, expressed on a cell surface, free in solution, or located 20 intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. One may measure, for example, the formulation of complexes between the agent being tested and a polypeptide of the present invention.

25 Thus, the present invention provides methods of screening for drugs or any other agents which affect activities mediated by the polypeptides of the present invention. These methods comprise contacting such an agent with a polypeptide of the present invention or a fragment thereof and assaying for the presence of a complex between the agent and the polypeptide or a fragment thereof, by methods well known in the art. In such a competitive 30 binding assay, the agents to screen are typically labeled. Following incubation, free agent is separated from that present in bound form, and the amount of free or uncomplexed label is a

measure of the ability of a particular agent to bind to the polypeptides of the present invention.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to the polypeptides of the present invention, and
5 is described in great detail in European Patent Application 84/03564, published on September 13, 1984, which is incorporated herein by reference herein. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with polypeptides of the present invention and washed. Bound polypeptides are then detected by methods well known
10 in the art. Purified polypeptides are coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies may be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding polypeptides of the present invention
15 specifically compete with a test compound for binding to the polypeptides or fragments thereof. In this manner, the antibodies are used to detect the presence of any peptide which shares one or more antigenic epitopes with a polypeptide of the invention.

Antisense And Ribozyme (Antagonists)

20 In specific embodiments, antagonists according to the present invention are nucleic acids corresponding to the sequences contained in SEQ ID NO:X, or the complementary strand thereof, and/or to nucleotide sequences contained in the cDNA contained in the related cDNA clone identified in Table 1. In one embodiment, antisense sequence is generated internally, by the organism, in another embodiment, the antisense sequence is separately
25 administered (see, for example, O'Connor, J., Neurochem. 56:560 (1991). Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Antisense technology can be used to control gene expression through antisense DNA or RNA, or through triple-helix formation. Antisense techniques are discussed for example, in Okano, J., Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense
30 Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Triple helix formation is discussed in, for instance, Lee et al., Nucleic Acids Research 6:3073 (1979); Cooney et al.,

Science 241:456 (1988); and Dervan et al., Science 251:1300 (1991). The methods are based on binding of a polynucleotide to a complementary DNA or RNA.

For example, the use of c-myc and c-myb antisense RNA constructs to inhibit the growth of the non-lymphocytic leukemia cell line HL-60 and other cell lines was previously described. (Wickstrom et al. (1988); Anfossi et al. (1989)). These experiments were performed in vitro by incubating cells with the oligoribonucleotide. A similar procedure for in vivo use is described in WO 91/15580. Briefly, a pair of oligonucleotides for a given antisense RNA is produced as follows: A sequence complimentary to the first 15 bases of the open reading frame is flanked by an EcoRI site on the 5' end and a HindIII site on the 3' end. Next, the pair of oligonucleotides is heated at 90°C for one minute and then annealed in 2X ligation buffer (20mM TRIS HCl pH 7.5, 10mM MgCl₂, 10MM dithiothreitol (DTT) and 0.2 mM ATP) and then ligated to the EcoRI/Hind III site of the retroviral vector PMV7 (WO 91/15580).

For example, the 5' coding portion of a polynucleotide that encodes the polypeptide of the present invention may be used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription thereby preventing transcription and the production of the receptor. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into receptor polypeptide.

In one embodiment, the antisense nucleic acid of the invention is produced intracellularly by transcription from an exogenous sequence. For example, a vector or a portion thereof, is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding the antisense nucleic acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in vertebrate cells. Expression of the sequence encoding the polypeptide of the present invention or fragments thereof, can be by any promoter known in the art to act in vertebrate, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, Nature 29:304-310 (1981), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., Cell 22:787-797

(1980), the herpes thymidine promoter (Wagner et al., Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445 (1981). the regulatory sequences of the metallothionein gene (Brinster, et al., Nature 296:39-42 (1982)), etc.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a gene of the present invention. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the larger the hybridizing nucleic acid, the more base mismatches with a RNA it may contain and still form a stable duplex (or triplex as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the message, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should work most efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have been shown to be effective at inhibiting translation of mRNAs as well. See generally, Wagner, R., 1994, Nature 372:333-335. Thus, oligonucleotides complementary to either the 5'- or 3'- non-translated, non-coding regions of polynucleotide sequences described herein could be used in an antisense approach to inhibit translation of endogenous mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are less efficient inhibitors of translation but could be used in accordance with the invention. Whether designed to hybridize to the 5'-, 3'- or coding region of mRNA of the present invention, antisense nucleic acids should be at least six nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In specific aspects the oligonucleotide is at least 10 nucleotides, at least 17 nucleotides, at least 25 nucleotides or at least 50 nucleotides.

The polynucleotides of the invention can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The

oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 5 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. WO88/09810, published December 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication No. WO89/10134, published April 25, 1988), hybridization-triggered cleavage agents. (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5:539-549). To this end, the 10 oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including, but not limited to, 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 15 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-20 D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

25 The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group including, but not limited to, a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet another embodiment, the antisense oligonucleotide is an a-anomeric oligonucleotide. An a-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual b-units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-0-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

Polynucleotides of the invention may be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides 10 may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc.

While antisense nucleotides complementary to the coding region sequence could be used, those complementary to the transcribed untranslated region are most preferred.

15 Potential antagonists according to the invention also include catalytic RNA, or a ribozyme (See, e.g., PCT International Publication WO 90/11364, published October 4, 1990; Sarver et al, Science 247:1222-1225 (1990). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by 20 flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, Nature 334:585-591 (1988). There are numerous potential hammerhead ribozyme cleavage sites within the nucleotide sequence of 25 SEQ ID NO:X. Preferably, the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

As in the antisense approach, the ribozymes of the invention can be composed of modified oligonucleotides (e.g. for improved stability, targeting, etc.) and should be delivered 30 to cells which express in vivo. DNA constructs encoding the ribozyme may be introduced into the cell in the same manner as described above for the introduction of antisense encoding DNA. A preferred method of delivery involves using a DNA construct "encoding" the

ribozyme under the control of a strong constitutive promoter, such as, for example, pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous messages and inhibit translation. Since ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

5 Antagonist/agonist compounds may be employed to inhibit the cell growth and proliferation effects of the polypeptides of the present invention on neoplastic cells and tissues, i.e. stimulation of angiogenesis of tumors, and, therefore, retard or prevent abnormal cellular growth and proliferation, for example, in tumor formation or growth.

10 The antagonist/agonist may also be employed to prevent hyper-vascular diseases, and prevent the proliferation of epithelial lens cells after extracapsular cataract surgery. Prevention of the mitogenic activity of the polypeptides of the present invention may also be desirous in cases such as restenosis after balloon angioplasty.

The antagonist/agonist may also be employed to prevent the growth of scar tissue during wound healing.

15 The antagonist/agonist may also be employed to treat the diseases described herein.

Thus, the invention provides a method of treating disorders or diseases, including but not limited to the disorders or diseases listed throughout this application, associated with overexpression of a polynucleotide of the present invention by administering to a patient (a) an antisense molecule directed to the polynucleotide of the present invention, and/or (b) a 20 ribozyme directed to the polynucleotide of the present invention.

Other Activities

A polypeptide, polynucleotide, agonist, or antagonist of the present invention, as a result of the ability to stimulate vascular endothelial cell growth, may be employed in 25 treatment for stimulating re-vascularization of ischemic tissues due to various disease conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions. The polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed to stimulate angiogenesis and limb regeneration, as discussed above.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may 30 also be employed for treating wounds due to injuries, burns, post-operative tissue repair, and ulcers since they are mitogenic to various cells of different origins, such as fibroblast cells

and skeletal muscle cells, and therefore, facilitate the repair or replacement of damaged or diseased tissue.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed stimulate neuronal growth and to treat and prevent neuronal damage which 5 occurs in certain neuronal disorders or neuro-degenerative conditions such as Alzheimer's disease, Parkinson's disease, and AIDS-related complex. A polypeptide, polynucleotide, agonist, or antagonist of the present invention may have the ability to stimulate chondrocyte growth, therefore, they may be employed to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts.

10 A polypeptide, polynucleotide, agonist, or antagonist of the present invention may be also be employed to prevent skin aging due to sunburn by stimulating keratinocyte growth.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed for preventing hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth. Along the same lines, a polypeptide, polynucleotide, 15 agonist, or antagonist of the present invention may be employed to stimulate growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed to maintain organs before transplantation or for supporting cell culture of 20 primary tissues. A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed for inducing tissue of mesodermal origin to differentiate in early embryos.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, 25 as discussed above, hematopoietic lineage.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be used to modulate mammalian characteristics. such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide, polynucleotide, agonist, or antagonist of the present 30 invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, cardiac rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity),
5 hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

10 The above-recited applications have uses in a wide variety of hosts. Such hosts include, but are not limited to, human, murine, rabbit, goat, guinea pig, camel, horse, mouse, rat, hamster, pig, micro-pig, chicken, goat, cow, sheep, dog, cat, non-human primate, and human. In specific embodiments, the host is a mouse, rabbit, goat, guinea pig, chicken, rat, hamster, pig, sheep, dog or cat. In preferred embodiments, the host is a mammal. In most
15 preferred embodiments, the host is a human.

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence
20 of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions
25 identified as "Start" and "End" in columns 7 and 8 as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

30 Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous

nucleotides in the nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

- A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X in the 5 range of positions identified as "Start" and "End" in columns 7 and 8 as defined for SEQ ID NO:X in Table 1.

- A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA 10 clone contained in the deposit.

- Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit, wherein said nucleic acid molecule which hybridizes does not 15 hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a cDNA clone contained in the deposit.

- Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence 20 which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of the cDNA in the related cDNA clone contained in the deposit.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of an open reading frame sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

- 25 Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

- A further preferred embodiment is an isolated nucleic acid molecule comprising a 30 nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

- A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

- Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

- A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

- Also preferred is the above method for identifying the species, tissue or cell type of a biological sample which comprises a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

- Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a nucleotide sequence of SEQ ID NO:X; or the cDNA contained in the related cDNA clone referenced in Table 1 which encodes a protein, wherein the method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence of the cDNA in the related cDNA clone contained in the deposit.
- 10 Also preferred is the above method for diagnosing a pathological condition which comprises a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.
- 15 Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit. The nucleic acid molecules can comprise DNA molecules or RNA molecules.
- 20 Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a DNA microarray or "chip" of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 40, 50, 100, 150, 200, 250, 300, 500, 1000, 2000, 3000 or 4000 nucleotide sequences, wherein at least one sequence in said DNA microarray or "chip" is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the cDNA clone referenced in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

5 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated polypeptide comprising an amino acid sequence at 10 least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated polypeptide comprising an amino acid sequence at 15 least 95% identical to the complete amino acid sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

20 Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a portion of said polypeptide encoded by the cDNA clone referenced in Table 1; a polypeptide encoded by SEQ ID NO:X; and/or the polypeptide sequence of SEQ ID NO:Y.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 25 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

30 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: a polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide 5 encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: a polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide 10 encoded by the cDNA in the related cDNA clone referenced in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

15 Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a 20 sequence selected from the group consisting of: a polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in 25 said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: 30 a polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a nucleic acid sequence identified in Table 1 encoding a polypeptide, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a

recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a human protein comprising an amino acid sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table I. The 10 isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a protein activity, which method comprises administering to such an individual a Therapeutic comprising an amount of an isolated polypeptide, polynucleotide, immunogenic fragment or analogue thereof, binding agent, antibody, or antigen binding fragment of the 15 claimed invention effective to increase the level of said protein activity in said individual.

Also preferred is a method of treatment of an individual in need of a decreased level of a protein activity, which method comprised administering to such an individual a Therapeutic comprising an amount of an isolated polypeptide, polynucleotide, immunogenic fragment or analogue thereof, binding agent, antibody, or antigen binding fragment of the 20 claimed invention effective to decrease the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

*Examples**Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample*

5

Each deposited cDNA clone is contained in a plasmid vector. Table 5 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The following correlates the related plasmid for each phage vector used in 10 constructing the cDNA library. For example, where a particular clone is identified in Table 5 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
15	Uni-Zap XR	pBluescript (pBS)
	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport I	pSport I
	pCMVSport 2.0	pCMVSport 2.0
20	pCMVSport 3.0	pCMVSport 3.0
	pCR®2.1	pCR®2.1
	Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128,256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988);	
25	Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the	
30		

orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

- Vectors pSport1, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an 5 ampicillin resistance gene and may be transformed into E. coli strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR®2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an 10 ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 5, as well as the corresponding plasmid vector sequences designated above.
- 15 The deposited material in the sample assigned the ATCC Deposit Number cited by reference to Table 2 and 5 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone referenced in Table 1.

TABLE 5

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HUKA HUKB HUKC HUKD HUKE HUKF HUKG	Human Uterine Cancer	Lambda ZAP II	LP01
HCNA HCNB	Human Colon	Lambda Zap II	LP01
HFFA	Human Fetal Brain. random primed	Lambda Zap II	LP01
HTWA	Resting T-Cell	Lambda ZAP II	LP01
HBQA	Early Stage Human Brain. random primed	Lambda ZAP II	LP01
HLMB HLMF HLMG HLMH HLMI HLMJ HLNIM HLMN	breast lymph node CDNA library	Lambda ZAP II	LP01
HCQA HCQB	human colon cancer	Lamda ZAP II	LP01
HMEA HMEC HMED HMEE HMEF HMEG HMEI HMEJ HMEK HMEL	Human Microvascular Endothelial Cells. fract. A	Lambda ZAP II	LP01
HUSA HUSC	Human Umbilical Vein Endothelial Cells. fract. A	Lambda ZAP II	LP01
HLQA HLQB	Hepatocellular Tumor	Lambda ZAP II	LP01
HHGA HHGB HHGC HHGD	Hemangiopericytoma	Lambda ZAP II	LP01
HSDM	Human Striatum Depression, re-rescue	Lambda ZAP II	LP01
HUSH	H Umbilical Vein Endothelial Cells, frac A. re-excision	Lambda ZAP II	LP01
HSGS	Salivary gland, subtracted	Lambda ZAP II	LP01
HFXA HFXB HFXC HFXD HFXE HFXF HFXG HFXH	Brain frontal cortex	Lambda ZAP II	LP01
HPQA HPQB HPQC	PERM TF274	Lambda ZAP II	LP01
HFXJ HFXK	Brain Frontal Cortex, re-excision	Lambda ZAP II	LP01
HCWA HCWB HCWC HCWD HCWE HCWF HCWG HCWH HCWI HCWJ HCWK	CD34 positive cells (Cord Blood)	ZAP Express	LP02
HCUA HCUB HCUC	CD34 depleted Buffy Coat (Cord Blood)	ZAP Express	LP02
HRSM	A-14 cell line	ZAP Express	LP02
HRSA	A1-CELL LINE	ZAP Express	LP02
HCUD HCUE HCUF HCUG HCUH HCUI	CD34 depleted Buffy Coat (Cord Blood). re-excision	ZAP Express	LP02
HBXE HBXF HBXG	H. Whole Brain #2. re-excision	ZAP Express	LP02
HRLM	L8 cell line	ZAP Express	LP02
HBXA HBXB HBXC HBXD	Human Whole Brain #2 - Oligo dT > 1.5Kb	ZAP Express	LP02
HUDA HUDP HUDC	Testes	ZAP Express	LP02
HHTM HHTN HHTO	H. hypothalamus. frac A;re-excision	ZAP Express	LP02
HHTL	H. hypothalamus. frac A	ZAP Express	LP02
HASA HASD	Human Adult Spleen	Uni-ZAP XR	LP03
HFKC HFKD HFKE HFKF HFKG	Human Fetal Kidney	Uni-ZAP XR	LP03
HE8A HE8B HE8C HE8D HE8E HE8F HE8M HE8N	Human 8 Week Whole Embryo	Uni-ZAP XR	LP03
HGBA HGBD HGBE HGBF HGBG HGBH HGBI	Human Gall Bladder	Uni-ZAP XR	LP03
HLHA HLHB HLHC HLHD HLHE	Human Fetal Lung III	Uni-ZAP XR	LP03

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HLHF HLHG HLHH HLHQ			
HPMA HPMB HPMC HPMD HPME HMPF HPMG HPMH	Human Placenta	Uni-ZAP XR	LP03
HPRA HPRB HPRC HPRD	Human Prostate	Uni-ZAP XR	LP03
HSIA HSIC HSID HSIE	Human Adult Small Intestine	Uni-ZAP XR	LP03
HTEA HTEB HTEC HTED HTEE HTEF HTEG HTEH HTEI HTEJ HTEK	Human Testes	Uni-ZAP XR	LP03
HTPA HTPB HTPC HTPD HTPE	Human Pancreas Tumor	Uni-ZAP XR	LP03
HTTA HTTB HTTC HTTD HTTE HTTF	Human Testes Tumor	Uni-ZAP XR	LP03
HAPA HAPB HAPC HAPM	Human Adult Pulmonary	Uni-ZAP XR	LP03
HETA HETB HETC HETD HETE HETF HETG HETH HETI	Human Endometrial Tumor	Uni-ZAP XR	LP03
HHFB HHFC HHFD HHFE HHFF HHFG HHFH HHFI	Human Fetal Heart	Uni-ZAP XR	LP03
HHPB HHPC HHPD HHPE HHPF HHPG HHPH	Human Hippocampus	Uni-ZAP XR	LP03
HCE1 HCE2 HCE3 HCE4 HCE5 HCEB HCEC HCED HCEE HCEF HCEG	Human Cerebellum	Uni-ZAP XR	LP03
HUVB HUVC HUVD HUVE	Human Umbilical Vein. Endo. remake	Uni-ZAP XR	LP03
HSTA HSTB HSTC HSTD	Human Skin Tumor	Uni-ZAP XR	LP03
HTAA HTAB HTAC HTAD HTAE	Human Activated T-Cells	Uni-ZAP XR	LP03
HFEA HFEB HFEC	Human Fetal Epithelium (Skin)	Uni-ZAP XR	LP03
HJPA HJPB HJPC HJPD	HUMAN JURKAT MEMBRANE BOUND POLYSOMES	Uni-ZAP XR	LP03
HESA	Human epithelioid sarcoma	Uni-Zap XR	LP03
HLTA HLTB HLTC HLTD HLTE HLTF	Human T-Cell Lymphoma	Uni-ZAP XR	LP03
HFTA HFTB HFTC HFTD	Human Fetal Dura Mater	Uni-ZAP XR	LP03
HRDA HRDB HRDC HRDD HRDE HRDF	Human Rhabdomyosarcoma	Uni-ZAP XR	LP03
HCAA HCAB HCAC	Cem cells cyclohexamide treated	Uni-ZAP XR	LP03
HRGA HRGB HRGC HRGD	Raji Cells. cyclohexamide treated	Uni-ZAP XR	LP03
HSUA HSUB HSUC HSUM	Supt Cells. cyclohexamide treated	Uni-ZAP XR	LP03
HT4A HT4C HT4D	Activated T-Cells, 12 hrs.	Uni-ZAP XR	LP03
HE9A HE9B HE9C HE9D HE9E HE9F HE9G HE9H HE9M HE9N	Nine Week Old Early Stage Human	Uni-ZAP XR	LP03
HATA HATB HATC HATD HATE	Human Adrenal Gland Tumor	Uni-ZAP XR	LP03
HT5A	Activated T-Cells. 24 hrs.	Uni-ZAP XR	LP03
HFGA HFGM	Human Fetal Brain	Uni-ZAP XR	LP03
HNEA HNEB HNEC HNED HNEE	Human Neutrophil	Uni-ZAP XR	LP03
HBGB HBGD	Human Primary Breast Cancer	Uni-ZAP XR	LP03
HBNA HBNB	Human Normal Breast	Uni-ZAP XR	LP03
HCAS	Cem Cells. cyclohexamide treated. subtra	Uni-ZAP XR	LP03
HHPS	Human Hippocampus. subtracted	pBS	LP03
HKCS HKCU	Human Colon Cancer. subtracted	pBS	LP03

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HRGS	Raji cells. cyclohexamide treated, subtracted	pBS	LP03
HSUT	Supt cells. cyclohexamide treated, differentially expressed	pBS	LP03
HT4S	Activated T-Cells. 12 hrs. subtracted	Uni-ZAP XR	LP03
HCDA HCDB HCDC HCDD HCDE	Human Chondrosarcoma	Uni-ZAP XR	LP03
HOAA HOAB HOAC	Human Osteosarcoma	Uni-ZAP XR	LP03
HTLA HTLB HTLC HTLD HTLE HTLF	Human adult testis, large inserts	Uni-ZAP XR	LP03
HLMA HLMC HLMD	Breast Lymph node cDNA library	Uni-ZAP XR	LP03
H6EA H6EB H6EC	HL-60. PMA 4H	Uni-ZAP XR	LP03
HTXA HTXB HTXC HTXD HTXE HTXF HTXG HTXH	Activated T-Cell (12hs)/Thiouridine labelledEco	Uni-ZAP XR	LP03
HNFA HNFB HNFC HNFD HNFE HNFF HNFG HNFH HNFJ	Human Neutrophil. Activated	Uni-ZAP XR	LP03
HTOB HTOC	HUMAN TONSILS. FRACTION 2	Uni-ZAP XR	LP03
HMGB	Human OB MG63 control fraction I	Uni-ZAP XR	LP03
HOPB	Human OB HOS control fraction I	Uni-ZAP XR	LP03
HORB	Human OB HOS treated (10 nM E2) fraction I	Uni-ZAP XR	LP03
HSV A HSV B HSV C	Human Chronic Synovitis	Uni-ZAP XR	LP03
HROA	HUMAN STOMACH	Uni-ZAP XR	LP03
HBJA HBJB HBJC HBJD HBJE HBJF HBJG HBJH HBJI HBJJ HBJK	HUMAN B CELL LYMPHOMA	Uni-ZAP XR	LP03
HCRA HCRB HCRC	human corpus colosum	Uni-ZAP XR	LP03
HODA HODB HODC HODD	human ovarian cancer	Uni-ZAP XR	LP03
HDSA	Dermatofibrosarcoma Protuberance	Uni-ZAP XR	LP03
HMWA HMWB HMWC HMWD HMWE HMWF HMWG HMWH HMWI HMWJ	Bone Marrow Cell Line (RS4;11)	Uni-ZAP XR	LP03
HSOA	stomach cancer (human)	Uni-ZAP XR	LP03
HERA	SKIN	Uni-ZAP XR	LP03
HMDA	Brain-medulloblastoma	Uni-ZAP XR	LP03
HGLA HGLB HGLD	Glioblastoma	Uni-ZAP XR	LP03
HEAA	H. Atrophic Endometrium	Uni-ZAP XR	LP03
HBCA HBCB	H. Lymph node breast Cancer	Uni-ZAP XR	LP03
HPWT	Human Prostate BPH, re-excision	Uni-ZAP XR	LP03
HFVG HFVH HFVI	Fetal Liver. subtraction II	pBS	LP03
HNFI	Human Neutrophils, Activated. re-excision	pBS	LP03
HBMB HBMC HBMD	Human Bone Marrow, re-excision	pBS	LP03
HKML HKMM HKMN	H. Kidney Medulla. re-excision	pBS	LP03
HKIX HKIY	H. Kidney Cortex. subtracted	pBS	LP03
HADT	H. Amygdala Depression. subtracted	pBS	LP03
H6AS	HL-60. untreated. subtracted	Uni-ZAP XR	LP03
H6ES	HL-60. PMA 4H. subtracted	Uni-ZAP XR	LP03
H6BS	HL-60. RA 4h. Subtracted	Uni-ZAP XR	LP03

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
H6CS	HL-60. PMA Id. subtracted	Uni-ZAP XR	LP03
HTXJ HTXK	Activated T-cell(12h)/Thiouridine-re-excision	Uni-ZAP XR	LP03
HMSA HMSB HMSC HMSCD HMSE HMSF HMSG HMSH HMSI HMSJ HMSK	Monocyte activated	Uni-ZAP XR	LP03
HAGA HAGB HAGC HAGD HAGE HAGF	Human Amygdala	Uni-ZAP XR	LP03
HSRA HSRA HSRE	STROMAL -OSTEOCLASTOMA	Uni-ZAP XR	LP03
HSRD HSRT HSRG HSRR	Human Osteoclastoma Stromal Cells - unamplified	Uni-ZAP XR	LP03
HSQA HSQB HSQC HSQD HSQE HSQF HSQG	Stromal cell TF274	Uni-ZAP XR	LP03
HSKA HSKB HSKC HSKD HSKE HSKF HSKZ	Smooth muscle. serum treated	Uni-ZAP XR	LP03
HSLA HSLB HSLC HSLD HSLE HSLF HSLG	Smooth muscle.control	Uni-ZAP XR	LP03
HSDA HSDD HSDE HSDF HSDG HSDH	Spinal cord	Uni-ZAP XR	LP03
HPWS	Prostate-BPH subtracted II	pBS	LP03
HSKW HSKX HSKY	Smooth Muscle- HASTE normalized	pBS	LP03
HFPB HFPC HFPD	H. Frontal cortex.epileptic:re-excision	Uni-ZAP XR	LP03
HSDI HSDJ HSDK	Spinal Cord. re-excision	Uni-ZAP XR	LP03
HSKN HSKO	Smooth Muscle Serum Treated, Norm	pBS	LP03
HSKG HSKH HSKI	Smooth muscle. serum induced.re-exc	pBS	LP03
HFCF HFCB HFCC HFCD HFCE	Human Fetal Brain	Uni-ZAP XR	LP04
HPTA HPTB HPTD	Human Pituitary	Uni-ZAP XR	LP04
HTHB HTHC HTHD	Human Thymus	Uni-ZAP XR	LP04
HE6B HE6C HE6D HE6E HE6F HE6G HE6S	Human Whole Six Week Old Embryo	Uni-ZAP XR	LP04
HSSA HSSB HSSC HSSD HSSE HSSF HSSG HSSH HSSI HSSJ HSSK	Human Synovial Sarcoma	Uni-ZAP XR	LP04
HE7T	7 Week Old Early Stage Human, subtracted	Uni-ZAP XR	LP04
HEPA HEPB HEPC	Human Epididymus	Uni-ZAP XR	LP04
HSNA HSNB HSNC HSNM HSNN	Human Synovium	Uni-ZAP XR	LP04
HPFB HPFC HPFD HPFE	Human Prostate Cancer. Stage C fraction	Uni-ZAP XR	LP04
HE2A HE2D HE2E HE2H HE2I HE2M HE2N HE2O	12 Week Old Early Stage Human	Uni-ZAP XR	LP04
HE2B HE2C HE2F HE2G HE2P HE2Q	12 Week Old Early Stage Human, II	Uni-ZAP XR	LP04
HPTT HPTU	Human Pituitary, subtracted	Uni-ZAP XR	LP04
HAUA HAUB HAUC	Amniotic Cells - TNF induced	Uni-ZAP XR	LP04
HAQA HAQB HAQC HAQD	Amniotic Cells - Primary Culture	Uni-ZAP XR	LP04
HWTA HWTB HWTC	Wilms tumor	Uni-ZAP XR	LP04
HBSD	Bone Cancer. re-excision	Uni-ZAP XR	LP04
HSGB	Salivary gland. re-excision	Uni-ZAP XR	LP04
HSJA HSJB HSJC	Smooth muscle-ILb induced	Uni-ZAP XR	LP04
HSXA HSXB HSXC HSXD	Human Substantia Nigra	Uni-ZAP XR	LP04

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HSHA HSHB HSHC	Smooth muscle. IL1b induced	Uni-ZAP XR	LP04
HOUA HOUB HOUC HOUD HOUE	Adipocytes	Uni-ZAP XR	LP04
HPWA HPWB HPWC HPWD HPWE	Prostate BPH	Uni-ZAP XR	LP04
HELA HELB HELC HELD HELE HELF HELG HELH	Endothelial cells-control	Uni-ZAP XR	LP04
HEMA HEMB HEMC HEMD HEME HEMF HEMG HEMH	Endothelial-induced	Uni-ZAP XR	LP04
HBIA HBIB HBIC	Human Brain. Striatum	Uni-ZAP XR	LP04
HHSA-HHSB-HHSC-HHSD-HHSE	Human-Hypothalamus:Schizophrenia	Uni-ZAP-XR	LP04
HNGA HNGB HNGC HNGD HNGE HNGF HNGG HNGH HNGI HNGJ	neutrophils control	Uni-ZAP XR	LP04
HNHA HNHB HNHC HNHD HNHE HNHF HNHG HNNH HNHI HNHJ	Neutrophils IL-1 and LPS induced	Uni-ZAP XR	LP04
HSDB HSDC	STRIATUM DEPRESSION	Uni-ZAP XR	LP04
HHPT	Hypothalamus	Uni-ZAP XR	LP04
HSAT HSAU HSAV HSAW HSAX HSAY HSAZ	Anergic T-cell	Uni-ZAP XR	LP04
HBMS HBMT HBMU HBMV HBMW HBMX	Bone marrow	Uni-ZAP XR	LP04
HOEA HOEB HOEC HOED HOEE HOEF HOEJ	Osteoblasts	Uni-ZAP XR	LP04
HAIA HAIB HAIC HAID HAIE HAIF	Epithelial-TNF α and INF induced	Uni-ZAP XR	LP04
HTGA HTGB HTGC HTGD	Apoptotic T-cell	Uni-ZAP XR	LP04
HMCA HMCB HMCC HMCD HMCE	Macrophage-oxLDL	Uni-ZAP XR	LP04
HMAA HMAB HMAC HMAD HMAE HMAF HMAG	Macrophage (GM-CSF treated)	Uni-ZAP XR	LP04
HPHA	Normal Prostate	Uni-ZAP XR	LP04
HPIA HPIB HPIC	LNCAP prostate cell line	Uni-ZAP XR	LP04
HPJA HPJB HPJC	PC3 Prostate cell line	Uni-ZAP XR	LP04
HOSE HOSF HOSG	Human Osteoclastoma, re-excision	Uni-ZAP XR	LP04
HTGE HTGF	Apoptotic T-cell. re-excision	Uni-ZAP XR	LP04
HMAJ HMAK	H Macrophage (GM-CSF treated). re-excision	Uni-ZAP XR	LP04
HACB HACC HACD	Human Adipose Tissue. re-excision	Uni-ZAP XR	LP04
HFPA	H. Frontal Cortex. Epileptic	Uni-ZAP XR	LP04
HFAA HFAB HFAC HFAD HFAE	Alzheimers, spongy change	Uni-ZAP XR	LP04
HFAM	Frontal Lobe. Dementia	Uni-ZAP XR	LP04
HMIA HMIB HMIC	Human Manic Depression Tissue	Uni-ZAP XR	LP04
HTSA HTSE HTSF HTSG HTSH	Human Thymus	pBS	LP05
HPBA HPBB HPBC HPBD HPBE	Human Pineal Gland	pBS	LP05
HSAA HSAB HSAC	HSA 172 Cells	pBS	LP05
HSBA HSBB HSBC HSBM	HSC172 cells	pBS	LP05
HJAA HJAB HJAC HJAD	Jurkat T-cell G1 phase	pBS	LP05
HJBA HJBB HJBC HJBD	Jurkat T-Cell, S phase	pBS	LP05
HAFA HAFB	Aorta endothelial cells + TNF- α	pBS	LP05
HAWA HAWB HAWC	Human White Adipose	pBS	LP05
HTNA HTNB	Human Thyroid	pBS	LP05

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HONA	Normal Ovary. Premenopausal	pBS	LP05
HARA HARB	Human Adult Retina	pBS	LP05
HLJA HLJB	Human Lung	pCMVSport 1	LP06
HOFM HOFN HOFO	H. Ovarian Tumor. II. OV5232	pCMVSport 2.0	LP07
HOGA HOGB HOGC	OV 10-3-95	pCMVSport 2.0	LP07
HCGL	CD34+cells. II	pCMVSport 2.0	LP07
HDLA	Hodgkin's Lymphoma I	pCMVSport 2.0	LP07
HDTA HDTB HDT C HDTD HDTE	Hodgkin's Lymphoma II	pCMVSport 2.0	LP07
HKAA HKAB HKAC HKAD HKAE	Keratinocyte	pCMVSport 2.0	LP07
HKAF HKAG HKAH			
HCIM	CAPFINDER. Crohn's Disease. lib 2	pCMVSport 2.0	LP07
HKAL	Keratinocyte. lib 2	pCMVSport 2.0	LP07
HKAT	Keratinocyte. lib 3	pCMVSport 2.0	LP07
HNDA	Nasal polyps	pCMVSport 2.0	LP07
HDRA	H. Primary Dendritic Cells.lib 3	pCMVSport 2.0	LP07
HOHA HOHB HOHC	Human Osteoblasts II	pCMVSport 2.0	LP07
HLDA HLDB HLDC	Liver. Hepatoma	pCMVSport 3.0	LP08
HLDN HLDO HLDP	Human Liver. normal	pCMVSport 3.0	LP08
HMTA	pBMC stimulated w/ poly I/C	pCMVSport 3.0	LP08
HNTA	NTERA2. control	pCMVSport 3.0	LP08
HDPA HDPB HDPC HDPD HDPF	Primary Dendritic Cells, lib 1	pCMVSport 3.0	LP08
HDPG HDPII HDPI HDPII HDPK			
HDPM HDPN HDPO HDPP	Primary Dendritic cells.frac 2	pCMVSport 3.0	LP08
HMUA HMUB HMUC	Myeloid Progenitor Cell Line	pCMVSport 3.0	LP08
HHEA HHEB HHEC HHED	T Cell helper I	pCMVSport 3.0	LP08
HHEM HHEN HHEO HHEP	T cell helper II	pCMVSport 3.0	LP08
HEQA HEQB HEQC	Human endometrial stromal cells	pCMVSport 3.0	LP08
HJMA HJMB	Human endometrial stromal cells-treated with progesterone	pCMVSport 3.0	LP08
HSWA HSWB HSWC	Human endometrial stromal cells-treated with estradiol	pCMVSport 3.0	LP08
HSYA HSYB HSYC	Human Thymus Stromal Cells	pCMVSport 3.0	LP08
HLWA HLWB HLWC	Human Placenta	pCMVSport 3.0	LP08
HRAA HRAB HRAC	Rejected Kidney, lib 4	pCMVSport 3.0	LP08
HMTM	PCR, pBMC I/C treated	PCRII	LP09
HMJA	H. Meningima, M6	pSport 1	LP10
HMKA HMKB HMKC HMKD	H. Meningima, M1	pSport 1	LP10
HMKE			
HUSG HUSI	Human umbilical vein endothelial cells, IL-4 induced	pSport 1	LP10
HUSX HUSY	Human Umbilical Vein Endothelial Cells. uninduced	pSport 1	LP10
HOFA	Ovarian Tumor I, OV5232	pSport 1	LP10
HCFA HCFB HCFC HCFC	T-Cell PHA 16 hrs	pSport 1	LP10
HCFL HCFM HCFN HCFO	T-Cell PHA 24 hrs	pSport 1	LP10
HADA HADC HADD HADE HADF	Human Adipose	pSport 1	LP10
HADG			

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HOVA HOVB HOVC	Human Ovary	pSport 1	LP10
HTWB HTWC HTWD HTWE HTWF	Resting T-Cell Library.II	pSport 1	LP10
HMMA	Spleen metastatic melanoma	pSport 1	LP10
HLYA HLYB HLYC HLYD HLYE	Spleen. Chronic lymphocytic leukemia	pSport 1	LP10
HCGA	CD34+ cell. I	pSport 1	LP10
HEOM HEON	Human Eosinophils	pSport 1	LP10
HTDA	Human Tonsil. Lib 3	pSport 1	LP10
HSPA	Salivary Gland. Lib.2	pSport 1	LP10
HCHA HCHB HCHC	Breast Cancer cell line. MDA 36	pSport 1	LP10
HCHM HCHN	Breast Cancer Cell line. angiogenic	pSport 1	LP10
HCIA	Crohn's Disease	pSport 1	LP10
HDAA HDAB HDAC	HEL cell line	pSport 1	LP10
HABA	Human Astrocyte	pSport 1	LP10
HUFA HUFB HUFC	Ulcerative Colitis	pSport 1	LP10
HNTM	NTERA2 + retinoic acid. 14 days	pSport 1	LP10
HDQA	Primary Dendritic cells.CapFinder2. frac 1	pSport 1	LP10
HDQM	Primary Dendritic Cells. CapFinder. frac 2	pSport 1	LP10
HLDX	Human Liver. normal.CapFinder	pSport 1	LP10
HULA HULB HULC	Human Dermal Endothelial Cells.untreated	pSport1	LP10
HUMA	Human Dermal Endothelial cells.treated	pSport1	LP10
HCJA	Human Stromal Endometrial fibroblasts. untreated	pSport1	LP10
HCJM	Human Stromal endometrial fibroblasts. treated w/ estradiol	pSport1	LP10
HEDA	Human Stromal endometrial fibroblasts. treated with progesterone	pSport1	LP10
HFNA	Human ovary tumor cell OV350721	pSport1	LP10
HKGA HKGB HKGC HKGD	Merkel Cells	pSport1	LP10
HISA HISB HISC	Pancreas Islet Cell Tumor	pSport1	LP10
HLSA	Skin. burned	pSport1	LP10
HBZA	Prostate.BPH. Lib 2	pSport 1	LP10
HBZS	Prostate BPH.Lib 2. subtracted	pSport 1	LP10
HFIA HFIB HFIC	Synovial Fibroblasts (control)	pSport 1	LP10
HFIH HFII HFII	Synovial hypoxia	pSport 1	LP10
HFIT HFIIU HFIV	Synovial IL-1/TNF stimulated	pSport 1	LP10
HGCA	Messangial cell. frac 1	pSport1	LP10
HMVA HMVB HMVC	Bone Marrow Stromal Cell. untreated	pSport1	LP10
HFIX HFIY HFIZ	Synovial Fibroblasts (III/TNF). subt	pSport1	LP10
HFOX HFOY HFOZ	Synovial hypoxia-RSF subtracted	pSport1	LP10
HMQA HMQB HMQC HMQD	Human Activated Monocytes	Uni-ZAP XR	LP11
HLIA HLJB HLIC	Human Liver	pCMVSport 1	LP012
HHBA HHBB HHBC HHBD HHBE	Human Heart	pCMVSport 1	LP012
HBBA HBBB	Human Brain	pCMVSport 1	LP012

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HLJA HLJB HLJC HLJD HLJE	Human Lung	pCMVSport 1	LP012
HOGA HOGB HOGC	Ovarian Tumor	pCMVSport 2.0	LP012
HTJM	Human Tonsils. Lib 2	pCMVSport 2.0	LP012
HAMF HAMG	KMH2	pCMVSport 3.0	LP012
HAJA HAJB HAJC	L428	pCMVSport 3.0	LP012
HWBA HWBB HWBC HWBD HWBE	Dendritic cells. pooled	pCMVSport 3.0	LP012
HWAA HWAB HWAC HWAD HWAE	Human Bone Marrow. treated	pCMVSport 3.0	LP012
HYAA HYAB HYAC	B Cell lymphoma	pCMVSport 3.0	LP012
HWHG HWHH HWHI	Healing groin wound, 6.5 hours post incision	pCMVSport 3.0	LP012
HWHP HWHQ HWHR	Healing groin wound; 7.5 hours post incision	pCMVSport 3.0	LP012
HARM	Healing groin wound - zero hr post-incision (control)	pCMVSport 3.0	LP012
HBIM	Olfactory epithelium: nasalcavity	pCMVSport 3.0	LP012
HWDA	Healing Abdomen wound: 70&90 min post incision	pCMVSport 3.0	LP012
HWEA	Healing Abdomen Wound;15 days post incision	pCMVSport 3.0	LP012
HWJA	Healing Abdomen Wound;21&29 days	pCMVSport 3.0	LP012
HNAL	Human Tongue. frac 2	pSport1	LP012
HMJA	H. Meningima, M6	pSport1	LP012
HMKA HMKB HMKC HMKD HMKE	H. Meningima, M1	pSport1	LP012
HOFA	Ovarian Tumor I. OV5232	pSport1	LP012
HCFA HCFB HCFC HCFD	T-Cell PHA 16 hrs	pSport1	LP012
HCFL HCFL HCFCN HCFO	T-Cell PHA 24 hrs	pSport1	LP012
HMMA HMMB HMMC	Spleen metastatic melanoma	pSport1	LP012
HTDA	Human Tonsil. Lib 3	pSport1	LP012
HDBA	Human Fetal Thymus	pSport1	LP012
HDUA	Pericardium	pSport1	LP012
HBZA	Prostate.BPH. Lib 2	pSport1	LP012
HWCA	Larynx tumor	pSport1	LP012
HWKA	Normal lung	pSport1	LP012
HSMB	Bone marrow stroma,treated	pSport1	LP012
HBHM	Normal trachea	pSport1	LP012
HLFC	Human Larynx	pSport1	LP012
HLRB	Siebben Polyposis	pSport1	LP012
HNIA	Mammary Gland	pSport1	LP012
HNJB	Palate carcinoma	pSport1	LP012
HNKA	Palate normal	pSport1	LP012
HMZA	Pharynx carcinoma	pSport1	LP012
HABG	Cheek Carcinoma	pSport1	LP012
HMZM	Pharynx Carcinoma	pSport1	LP012
HDRM	Larynx Carcinoma	pSport1	LP012
HVAA	Pancreas normal PCA4 No	pSport1	LP012
HICA	Tongue carcinoma	pSport1	LP012

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HUKA HUKB HUKC HUKD HUKE	Human Uterine Cancer	Lambda ZAP II	LP013
HFFA	Human Fetal Brain. random primed	Lambda ZAP II	LP013
HTUA	Activated T-cell labeled with 4-thiouracil	Lambda ZAP II	LP013
HBQA	Early Stage Human Brain. random primed	Lambda ZAP II	LP013
HMEB	Human microvascular Endothelial cells. fract. B	Lambda ZAP II	LP013
HUSH	Human Umbilical Vein Endothelial cells. fract. A. re-excision	Lambda ZAP II	LP013
HLQC HLQD	Hepatocellular tumor. re-excision	Lambda ZAP II	LP013
HTWJ HTWK HTWL	Resting T-cell. re-excision	Lambda ZAP II	LP013
HF6S	Human Whole 6 week Old Embryo (II). subl	pBluescript	LP013
HHPS	Human Hippocampus. subtracted	pBluescript	LP013
HL1S	LNCAP. differential expression	pBluescript	LP013
HLHS HLHT	Early Stage Human Lung. Subtracted	pBluescript	LP013
HSUS	Supt cells. cyclohexamide treated. subtracted	pBluescript	LP013
HSUT	Supt cells, cyclohexamide treated. differentially expressed	pBluescript	LP013
HSDS	H. Striatum Depression. subtracted	pBluescript	LP013
HPTZ	Human Pituitary. Subtracted VII	pBluescript	LP013
HSDX	H. Striatum Depression. subl II	pBluescript	LP013
HSDZ	H. Striatum Depression. subl	pBluescript	LP013
HPBA HPBB HPBC HPBD HPBE	Human Pineal Gland	pBluescript SK-	LP013
HRTA	Colorectal Tumor	pBluescript SK-	LP013
HSBA HSBB HSBC HSBM	HSC172 cells	pBluescript SK-	LP013
HJAA HJAB HJAC HJAD	Jurkat T-cell G1 phase	pBluescript SK-	LP013
HJBA HJBB HJBC HJBD	Jurkat T-cell. S1 phase	pBluescript SK-	LP013
HTNA HTNB	Human Thyroid	pBluescript SK-	LP013
HAHA HAHB	Human Adult Heart	Uni-ZAP XR	LP013
HE6A	Whole 6 week Old Embryo	Uni-ZAP XR	LP013
HFCA HFCB HFCC HFCD HFCE	Human Fetal Brain	Uni-ZAP XR	LP013
HFKC HFKD HFKE HFKF HKFG	Human Fetal Kidney	Uni-ZAP XR	LP013
HGBA HGBD HGBE HGBF HGBG	Human Gall Bladder	Uni-ZAP XR	LP013
HPRA HPRB HPRC HPRD	Human Prostate	Uni-ZAP XR	LP013
HTEA HTEB HTEC HTED HTEE	Human Testes	Uni-ZAP XR	LP013
HTTA HTTB HTTC HTTD HTTE	Human Testes Tumor	Uni-ZAP XR	LP013
HYBA HYBB	Human Fetal Bone	Uni-ZAP XR	LP013
HFLA	Human Fetal Liver	Uni-ZAP XR	LP013
HHFB HHFC HHFD HHFE HHFF	Human Fetal Heart	Uni-ZAP XR	LP013
HUVB HUVC HUVD HUVE	Human Umbilical Vein. End. remake	Uni-ZAP XR	LP013
HTHB HTHC HTHD	Human Thymus	Uni-ZAP XR	LP013
HSTA HSTB HSTC HSTD	Human Skin Tumor	Uni-ZAP XR	LP013
HTAA HTAB HTAC HTAD HTAE	Human Activated T-cells	Uni-ZAP XR	LP013
HFEA HFEB HFEC	Human Fetal Epithelium (skin)	Uni-ZAP XR	LP013
HJPA HJPB HJPC HJPD	Human Jurkat Membrane Bound Polysomes	Uni-ZAP XR	LP013
HESA	Human Epithelioid Sarcoma	Uni-ZAP XR	LP013

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HALS	Human Adult Liver. Subtracted	Uni-ZAP XR	LP013
HFTA HFTB HFTC HFTD	Human Fetal Dura Mater	Uni-ZAP XR	LP013
HCAA HCAB HCAC	Cem cells. cyclohexamide treated	Uni-ZAP XR	LP013
HRGA HRGB HRGC HRGD	Raji Cells. cyclohexamide treated	Uni-ZAP XR	LP013
HE9A HE9B HE9C HE9D HE9E	Nine Week Old Early Stage Human	Uni-ZAP XR	LP013
HSFA	Human Fibrosarcoma	Uni-ZAP XR	LP013
HATA HATB HATC HATD HATE	Human Adrenal Gland Tumor	Uni-ZAP XR	LP013
HTRA	Human Trachea Tumor	Uni-ZAP XR	LP013
HE2A HE2D HE2E HE2H HE2I	I2-Week Old-Early Stage Human	Uni-ZAP XR	LP013
HE2B HE2C HE2F HE2G HE2P	I2 Week Old Early Stage Human. II	Uni-ZAP XR	LP013
HNEA HNEB HNEC HNED HNEE	Human Neutrophil	Uni-ZAP XR	LP013
HBGA	Human Primary Breast Cancer	Uni-ZAP XR	LP013
HPTS HPTT HPTU	Human Pituitary. subtracted	Uni-ZAP XR	LP013
HMQA HMQB HMQC HMQD	Human Activated Monocytes	Uni-ZAP XR	LP013
HOAA HOAB HOAC	Human Osteosarcoma	Uni-ZAP XR	LP013
HTOA HTOD HTOE HTOF HTOG	human tonsils	Uni-ZAP XR	LP013
HMGB	Human OB MG63 control fraction I	Uni-ZAP XR	LP013
HOPB	Human OB HOS control fraction I	Uni-ZAP XR	LP013
HOQB	Human OB HOS treated (1 nM E2) fraction I	Uni-ZAP XR	LP013
HAUA HAUB HAUC	Amniotic Cells - TNF induced	Uni-ZAP XR	LP013
HAQA HAQB HAQC HAQD	Amniotic Cells - Primary Culture	Uni-ZAP XR	LP013
HROA HROC	HUMAN STOMACH	Uni-ZAP XR	LP013
HBJA HBJB HBJC HBJD HBJE	HUMAN B CELL LYMPHOMA	Uni-ZAP XR	LP013
HOYA HODB HODC HODD	human ovarian cancer	Uni-ZAP XR	LP013
HCPA	Corpus Callosum	Uni-ZAP XR	LP013
HSOA	stomach cancer (human)	Uni-ZAP XR	LP013
HERA	SKIN	Uni-ZAP XR	LP013
HMDA	Brain-medulloblastoma	Uni-ZAP XR	LP013
HGLA HGLB HGLD	Glioblastoma	Uni-ZAP XR	LP013
HWTA HWTB HWTC	wilm's tumor	Uni-ZAP XR	LP013
HEAA	H. Atrophic Endometrium	Uni-ZAP XR	LP013
HAPN HAPO HAPP HAPQ HAPR	Human Adult Pulmonary:re-excision	Uni-ZAP XR	LP013
HLTG HLTH	Human T-cell lymphoma:re-excision	Uni-ZAP XR	LP013
HAHC HAHD HAHE	Human Adult Heart:re-excision	Uni-ZAP XR	LP013
HAGA HAGB HAGC HAGD HAGE	Human Amygdala	Uni-ZAP XR	LP013
HSJA HSJB HSJC	Smooth muscle-ILb induced	Uni-ZAP XR	LP013
HSHA HSHB HSHC	Smooth muscle, IL1b induced	Uni-ZAP XR	LP013
HPWA HPWB HPWC HPWD HPWE	Prostate BPH	Uni-ZAP XR	LP013
HPIA HPIB HPIC	LNCAP prostate cell line	Uni-ZAP XR	LP013
HPJA HPJB HPJC	PC3 Prostate cell line	Uni-ZAP XR	LP013
HBTA	Bone Marrow Stroma, TNF&LPS ind	Uni-ZAP XR	LP013
HMCF HMCG HMCH HMCI HMCJ	Macrophage-oxLDL; re-excision	Uni-ZAP XR	LP013
HAGG HAGH HAGI	Human Amygdala:re-excision	Uni-ZAP XR	LP013
HACA	H. Adipose Tissue	Uni-ZAP XR	LP013
HKFB	K562 + PMA (36 hrs).re-excision	ZAP Express	LP013
HCWT HCWU HCWV	CD34 positive cells (cord blood).re-ex	ZAP Express	LP013

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HBWA	Whole brain	ZAP Express	LP013
HBXA HBXB HBXC HBXD	Human Whole Brain #2 - Oligo dT > 1.5Kb	ZAP Express	LP013
HAVM	Temporal cortex-Alzheimmer	pT-Adv	LP014
HAVT	Hippocampus. Alzheimer Subtracted	pT-Adv	LP014
HHAS	CHME Cell Line	Uni-ZAP XR	LP014
HAJR	Larynx normal	pSport 1	LP014
HWLE HWLF HWLG HWLH	Colon Normal	pSport 1	LP014
HCRM HCRN.HCRO	Colon.Carcinoma	pSport 1	LP014
HWLI HWLJ HWLK	Colon Normal	pSport 1	LP014
HWLQ HWLR HWLS HWLT	Colon Tumor	pSport 1	LP014
HBFM	Gastrocnemius Muscle	pSport 1	LP014
HBOD HBOE	Quadriceps Muscle	pSport 1	LP014
HBKD HBKE	Soleus Muscle	pSport 1	LP014
HCCM	Pancreatic Langerhans	pSport 1	LP014
HWGA	Larynx carcinoma	pSport 1	LP014
HWGM HWGN	Larynx carcinoma	pSport 1	LP014
HWLA HWLB HWLC	Normal colon	pSport 1	LP014
HWLM HWLN	Colon Tumor	pSport 1	LP014
HVAM HVAN HVAO	Pancreas Tumor	pSport 1	LP014
HWGQ	Larynx carcinoma	pSport 1	LP014
HAQM HAQN	Salivary Gland	pSport 1	LP014
HASM	Stomach; normal	pSport 1	LP014
HBCM	Uterus; normal	pSport 1	LP014
HCDM	Testis; normal	pSport 1	LP014
HDJM	Brain; normal	pSport 1	LP014
HEFM	Adrenal Gland;normal	pSport 1	LP014
HBAA	Rectum normal	pSport 1	LP014
HFDM	Rectum tumour	pSport 1	LP014
HGAM	Colon, normal	pSport 1	LP014
HHMM	Colon. tumour	pSport 1	LP014
HCLB HCLC	Human Lung Cancer	Lambda Zap II	LP015
HRLA	L1 Cell line	ZAP Express	LP015
HHAM	Hypothalamus. Alzheimer's	pCMVSport 3.0	LP015
HKBA	Ku 812F Basophils Line	pSport 1	LP015
HS2S	Saos2, Dexamethosome Treated	pSport 1	LP016
HASA	Lung Carcinoma A549 TNFalpha activated	pSport 1	LP016
HTFM	TF-1 Cell Line GM-CSF Treated	pSport 1	LP016
HYAS	Thyroid Tumour	pSport 1	LP016
HUTS	Larynx Normal	pSport 1	LP016
HXOA	Larynx Tumor	pSport 1	LP016
HEAH	Ea.hy.926 cell line	pSport 1	LP016
HINA	Adenocarcinoma Human	pSport 1	LP016
HRMA	Lung Mesothelium	pSport 1	LP016
HLCL	Human Pre-Differentiated Adipocytes	Uni-Zap XR	LP017
HS2A	Saos2 Cells	pSport 1	LP020

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HS2I	Saos2 Cells: Vitamin D3 Treated	pSport I	LP020
HUCM	CHME Cell Line, untreated	pSport I	LP020
HEPN	Aryepiglottis Normal	pSport I	LP020
HPSN	Sinus Piniformis Tumour	pSport I	LP020
HNSA	Stomach Normal	pSport I	LP020
HNSM	Stomach Tumour	pSport I	LP020
HNLA	Liver Normal Met5No	pSport I	LP020
HUTA	Liver Tumour Met 5 Tu	pSport I	LP020
HOCN	Colon Normal	pSport I	LP020
HOCT	Colon Tumor	pSport I	LP020
HTNT	Tongue Tumour	pSport I	LP020
HLXN	Larynx Normal	pSport I	LP020
HLXT	Larynx Tumour	pSport I	LP020
HTYN	Thymus	pSport I	LP020
HPLN	Placenta	pSport I	LP020
HTNG	Tongue Normal	pSport I	LP020
HZAA	Thyroid Normal (SDCA2 No)	pSport I	LP020
HWES	Thyroid Thyroiditis	pSport I	LP020
HFHD	Ficoll Human Stromal Cells, 5Fu treated	pTrip1Ex2	LP021
HFHM.HFHN	Ficoll Human Stromal Cells, Untreated	pTrip1Ex2	LP021
HPCI	Hep G2 Cells, lambda library	lambda Zap-CMV XR	LP021
HBCA,HBCB.HBCC	H. Lymph node breast Cancer	Uni-ZAP XR	LP021
HCOK	Chondrocytes	pSPORT1	LP022
HDCA. HDCB. HDCC	Dendritic Cells From CD34 Cells	pSPORT1	LP022
HDMA. HDMB	CD40 activated monocyte dendritic cells	pSPORT1	LP022
HDDM. HDDN. HDDO	LPS activated derived dendritic cells	pSPORT1	LP022
HPCR	Hep G2 Cells, PCR library	lambda Zap-CMV XR	LP022
HAAA, HAAB, HAAC	Lung, Cancer (4005313A3): Invasive Poorly Differentiated Lung Adenocarcinoma	pSPORT1	LP022
HIPA. HIPB. HIPC	Lung, Cancer (4005163 B7): Invasive, Poorly Diff. Adenocarcinoma, Metastatic	pSPORT1	LP022
HOOH, HOOI	Ovary. Cancer: (4004562 B6) Papillary Serous Cystic Neoplasm. Low Malignant Pot	pSPORT1	LP022
HIDA	Lung, Normal: (4005313 B1)	pSPORT1	LP022
HUJA.HUJB.HUJC.HUJD.HUJE	B-Cells	pCMVSport 3.0	LP022
HNDA.HNOB.HNOC.HNOD	Ovary. Normal: (9805C040R)	pSPORT1	LP022
HNLM	Lung, Normal: (4005313 B1)	pSPORT1	LP022
HSCL	Stromal Cells	pSPORT1	LP022
HAAX	Lung, Cancer: (4005313 A3) Invasive Poorly-differentiated Metastatic lung adenocarcinoma	pSPORT1	LP022
HUUA.HUUB.HUUC.HUUD	B-cells (unstimulated)	pTrip1Ex2	LP022
HWWA.HWWB.HWWC.HWWD.HWWE.HWWF.HWWG	B-cells (stimulated)	pSPORT1	LP022
HCCC	Colon. Cancer: (9808C064R)	pCMVSport 3.0	LP023

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HPDO HPDP HPDQ HPDR HPD	Ovary, Cancer (9809C332): Poorly differentiated adenocarcinoma	pSport 1	LP023
HPCO HPCP HPCQ HPCT	Ovary, Cancer (15395A1F): Grade II Papillary Carcinoma	pSport 1	LP023
HOCM HOCH OCO HOCQ	Ovary, Cancer: (15799A1F) Poorly differentiated carcinoma	pSport 1	LP023
HCBM HCBN HCBO	Breast, Cancer: (4004943 A5)	pSport 1	LP023
HNBT HNBH HNBV	Breast, Normal: (4005522B2)	pSport 1	LP023
HBCP-HBCQ	Breast, Cancer: (4005522.A2)	pSport 1	LP023
HBCJ	Breast, Cancer: (9806C012R)	pSport 1	LP023
HSAM HSAN	Stromal cells 3.88	pSport 1	LP023
HVCA HVCB HVCC HVCD	Ovary, Cancer: (4004332 A2)	pSport 1	LP023
HSCK HSEN HSEO	Stromal cells (HBM3.18)	pSport 1	LP023
HSCP HSCQ	stromal cell clone 2.5	pSport 1	LP023
HUXA	Breast Cancer: (4005385 A2)	pSport 1	LP023
HCOM HCON HCOO HCOP HCOQ	Ovary, Cancer (4004650 A3): Well-Differentiated Micropapillary Serous Carcinoma	pSport 1	LP023
HBNM	Breast, Cancer: (9802C020E)	pSport 1	LP023
HVVA HVVB HVVC HVVD HVVE	Human Bone Marrow, treated	pSport 1	LP023

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 5. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to the nucleotide sequence of SEQ ID NO:X.

5 Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ^{32}P - γ -ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid
10 mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using
15 Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the
20 nucleotide sequence of SEQ ID NO:X are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 μl of reaction mixture with 0.5 ug of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl₂, 0.01% (w/v) gelatin, 20 μM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of
25 Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA
30 product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not

limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993).)

5 Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full
10 length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the
15 RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis
20 using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

25

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using
primers selected for the sequence corresponding to SEQ ID NO:X, according to the method
30 described in Example 1. (See also, Sambrook.)

Example 3: Tissue specific expression analysis

The Human Genome Sciences, Inc. (HGS) database is derived from sequencing tissue specific cDNA libraries. Libraries generated from a particular tissue are selected and the 5 specific tissue expression pattern of EST groups or assembled contigs within these libraries is determined by comparison of the expression patterns of those groups or contigs within the entire database. ESTs which show tissue specific expression are selected.

The original clone from which the specific EST sequence was generated, is obtained from the catalogued library of clones and the insert amplified by PCR using methods known 10 in the art. The PCR product is denatured then transferred in 96 well format to a nylon membrane (Schleicher and Scheull) generating an array filter of tissue specific clones. Housekeeping genes, maize genes, and known tissue specific genes are included on the filters. These targets can be used in signal normalization and to validate assay sensitivity. Additional targets are included to monitor probe length and specificity of hybridization.

15 Radioactively labeled hybridization probes are generated by first strand cDNA synthesis per the manufacturer's instructions (Life Technologies) from mRNA/RNA samples prepared from the specific tissue being analyzed. The hybridization probes are purified by gel exclusion chromatography, quantitated, and hybridized with the array filters in hybridization bottles at 65°C overnight. The filters are washed under stringent conditions and signals are 20 captured using a Fuji phosphorimager.

Data is extracted using AIS software and following background subtraction, signal normalization is performed. This includes a normalization of filter-wide expression levels between different experimental runs. Genes that are differentially expressed in the tissue of interest are identified and the full length sequence of these clones is generated.

25

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5' end of 30 SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute

cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

Example 5: Bacterial Expression of a Polypeptide

A polynucleotide encoding a polypeptide of the present invention is amplified using 10 PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial 15 expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^R), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is 20 ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^R). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is 25 isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture 30 in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM immidazole. Immidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl.

20 The purified protein is stored at 4°C or frozen at -80°C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (lacIq). The origin of replication (oriC) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, 30 BamHI, Xhol, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction

sites for NdeI (5' primer) and XbaI, BamHI, Xhol, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express
5 protein in a bacterial system.

Example 6: Purification of a Polypeptide from an Inclusion Body

The following alternative method can be used to purify a polypeptide expressed in *E*
10 *coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell
15 paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then
20 mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is
25 discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous
30 stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column 5 is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns 10 of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging 15 from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from 20 Commassie blue stained 16% SDS-PAGE gel when 5 µg of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System

25

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of 30 the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak Drosophila promoter in the same orientation, followed by the

polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as 5 pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the 10 AUG initiation codon, is amplified using the PCR protocol described in Example 1. If a naturally occurring signal sequence is used to produce the polypeptide of the present invention, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and 15 Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

20 The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.).

25 The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

30 Five µg of a plasmid containing the polynucleotide is co-transfected with 1.0 µg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc.

Natl. Acad. Sci. USA 84:7413-7417 (1987). One μ g of BaculoGold™ virus DNA and 5 μ g of the plasmid are mixed in a sterile well of a microtiter plate containing 50 μ l of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μ l Lipofectin plus 90 μ l Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 μ l of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 μ Ci of 35 S-methionine and 5 μ Ci 35 S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

Example 8: Expression of a Polypeptide in Mammalian Cells

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSport 2.0, and pCMVSport 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as DHFR, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g.; Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 5 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If a naturally occurring signal sequence is used to produce the polypeptide of the present invention, the vector does not need a second signal peptide. 15 Alternatively, if a naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

20 The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

25 Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five µg of the expression plasmid pC6 or pC4 is cotransfected with 0.5 µg of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM 30 supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones

are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 µM, 2 µM, 5 µM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 µM. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

10

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., 15 Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion 20 proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using 25 primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, 30 the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without

a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the polypeptide of the present invention, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous 5 signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

GGGATCCGGAGCCCAAATCTTCTGACAAAACTCACACATGCCACC GTGCCAG
CACCTGAATTGAGGGTGCACCGTCAGTCTCCTCTTCCCCAAAACCCAAGGA
10 CACCCTCATGATCTCCGGACTCCTGAGGTACATGCGTGGTGGACGTAAGC
CACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAT
AATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC
AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC
AAGGTCTCCAACAAAGCCCTCCAACCCCCATCGAGAAAACCATCTCAAAGCC
15 AAAGGGCAGCCCCGAGAACCAACAGGTGTACACCCTGCCCATCCGGATGAG
CTGACCAAGAACCAAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAAGC
GACATGCCGTGGAGTGGAGAGCAATGGCAGCCGGAGAACAACTACAAGAC
CACGCCTCCGTGGACTCCGACGGCTCCTCTACAGCAAGCTCACC
GTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTCTCATGCTCCGTGATGCAT
20 GAGGCTCTGCACAACCAACTACACGCAGAACAGCCTCCCTGTCTCCGGTAAAT
GAGTGCGACGGCCCGACTCTAGAGGAT (SEQ ID NO:1547)

Example 10: Production of an Antibody from a Polypeptide

25 a) Hybridoma Technology

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) As one example of such methods, cells expressing polypeptide of the present invention are administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of polypeptide 30 of the present invention is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

Monoclonal antibodies specific for polypeptide of the present invention are prepared using hybridoma technology. (Kohler et al., *Nature* 256:495 (1975); Kohler et al., *Eur. J. Immunol.* 6:511 (1976); Kohler et al., *Eur. J. Immunol.* 6:292 (1976); Hammerling et al., in: *Monoclonal Antibodies and T-Cell Hybridomas*, Elsevier, N.Y., pp. 563-681 (1981)). In general, an animal (preferably a mouse) is immunized with polypeptide of the present invention or, more preferably, with a secreted polypeptide of the present invention-expressing cell. Such polypeptide-expressing cells are cultured in any suitable tissue culture medium, preferably in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (*Gastroenterology* 80:225-232 (1981)). The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide of the present invention.

Alternatively, additional antibodies capable of binding to polypeptide of the present invention can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the polypeptide of the present invention-specific antibody can be blocked by polypeptide of the present invention. Such antibodies comprise anti-idiotypic antibodies to the polypeptide of the present invention-specific antibody and are used to immunize an animal to induce formation of further polypeptide of the present invention-specific antibodies.

For *in vivo* use of antibodies in humans, an antibody is "humanized". Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric and humanized

antibodies are known in the art and are discussed herein. (See, for review, Morrison, *Science* 229:1202 (1985); Oi et al., *BioTechniques* 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulian et al., *Nature* 312:643 (1984); Neuberger et al., *Nature* 314:268 (1985).)

b) Isolation Of Antibody Fragments Directed Against Polypeptide of the Present Invention From A Library Of scFvs

Naturally occurring V-genes isolated from human PBLs are constructed into a library 10 of antibody fragments which contain reactivities against polypeptide of the present invention to which the donor may or may not have been exposed (see e.g., U.S. Patent 5,885,793 incorporated herein by reference in its entirety).

Rescue of the Library. A library of scFvs is constructed from the RNA of human PBLs as described in PCT publication WO 92/01047. To rescue phage displaying antibody 15 fragments, approximately 109 E. coli harboring the phagemid are used to inoculate 50 ml of 2xTY containing 1% glucose and 100 µg/ml of ampicillin (2xTY-AMP-GLU) and grown to an O.D. of 0.8 with shaking. Five ml of this culture is used to innoculate 50 ml of 2xTY-AMP-GLU, 2 x 10⁸ TU of delta gene 3 helper (M13 delta gene III, see PCT publication WO 92/01047) are added and the culture incubated at 37°C for 45 minutes without shaking and 20 then at 37°C for 45 minutes with shaking. The culture is centrifuged at 4000 r.p.m. for 10 min. and the pellet resuspended in 2 liters of 2xTY containing 100 µg/ml ampicillin and 50 µg/ml kanamycin and grown overnight. Phage are prepared as described in PCT publication WO 92/01047.

M13 delta gene III is prepared as follows: M13 delta gene III helper phage does not 25 encode gene III protein, hence the phage(mid) displaying antibody fragments have a greater avidity of binding to antigen. Infectious M13 delta gene III particles are made by growing the helper phage in cells harboring a pUC19 derivative supplying the wild type gene III protein during phage morphogenesis. The culture is incubated for 1 hour at 37° C without shaking and then for a further hour at 37°C with shaking. Cells are spun down (IEC-Centra 30 8,400 r.p.m. for 10 min), resuspended in 300 ml 2xTY broth containing 100 µg ampicillin/ml and 25 µg kanamycin/ml (2xTY-AMP-KAN) and grown overnight, shaking at 37°C. Phage particles are purified and concentrated from the culture medium by two PEG-precipitations

(Sambrook et al., 1990), resuspended in 2 ml PBS and passed through a 0.45 µm filter (Minisart NML; Sartorius) to give a final concentration of approximately 10¹³ transducing units/ml (ampicillin-resistant clones).

Panning of the Library. Immunotubes (Nunc) are coated overnight in PBS with 4 ml of either 100 µg/ml or 10 µg/ml of a polypeptide of the present invention. Tubes are blocked with 2% Marvel-PBS for 2 hours at 37°C and then washed 3 times in PBS. Approximately 10¹³ TU of phage is applied to the tube and incubated for 30 minutes at room temperature tumbling on an over and under turntable and then left to stand for another 1.5 hours. Tubes are washed 10 times with PBS 0.1% Tween-20 and 10 times with PBS. Phage are eluted by adding 1 ml of 100 mM triethylamine and rotating 15 minutes on an under and over turntable after which the solution is immediately neutralized with 0.5 ml of 1.0M Tris-HCl, pH 7.4. Phage are then used to infect 10 ml of mid-log E. coli TG1 by incubating eluted phage with bacteria for 30 minutes at 37°C. The E. coli are then plated on TYE plates containing 1% glucose and 100 µg/ml ampicillin. The resulting bacterial library is then rescued with delta gene 3 helper phage as described above to prepare phage for a subsequent round of selection. This process is then repeated for a total of 4 rounds of affinity purification with tube-washing increased to 20 times with PBS, 0.1% Tween-20 and 20 times with PBS for rounds 3 and 4.

Characterization of Binders. Eluted phage from the 3rd and 4th rounds of selection are used to infect E. coli HB 2151 and soluble scFv is produced (Marks, et al., 1991) from single colonies for assay. ELISAs are performed with microtitre plates coated with either 10 pg/ml of the polypeptide of the present invention in 50 mM bicarbonate pH 9.6. Clones positive in ELISA are further characterized by PCR fingerprinting (see, e.g., PCT publication WO 92/01047) and then by sequencing. These ELISA positive clones may also be further characterized by techniques known in the art, such as, for example, epitope mapping, binding affinity, receptor signal transduction, ability to block or competitively inhibit antibody/antigen binding, and competitive agonistic or antagonistic activity.

Example 11: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

30

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is isolated. cDNA is then generated from these RNA

samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X; and/or the nucleotide sequence of the related cDNA in the cDNA clone contained in a deposited library. Suggested PCR conditions consist of 35 cycles at 95 degrees C for 30
5 seconds; 60-120 seconds at 52-58 degrees C; and 60-120 seconds at 70 degrees C, using buffer solutions described in Sidransky et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTTM Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR products
10 analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton et al., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected
15 individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenin-deoxy-uridine 5'-triphosphate (Boehringer Manheim), and FISH performed as described in Johnson et al., Methods Cell Biol. 35:73-99 (1991).
20 Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination
25 with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions,
30 deletions, and translocations. These alterations are used as a diagnostic marker for an associated disease.

Example 12: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for 5 a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal 10 or polyclonal and are produced by the method described in Example 10. The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded 15 polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate 20 (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

25

Example 13: Formulation

The invention also provides methods of treatment and/or prevention of diseases or disorders (such as, for example, any one or more of the diseases or disorders disclosed 30 herein) by administration to a subject of an effective amount of a Therapeutic. By therapeutic is meant a polynucleotides or polypeptides of the invention (including fragments and variants), agonists or antagonists thereof, and/or antibodies thereto, in combination with

a pharmaceutically acceptable carrier type (e.g., a sterile carrier).

The Therapeutic will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the Therapeutic alone), the site of delivery, the 5 method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of the Therapeutic administered parenterally per dose will be in the range of about 1 ug/kg/day to 10 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the Therapeutic is typically administered at a dose rate of about 1 ug/kg/hour to about 50 ug/kg/hour, either by 1-4 injections per day or by continuous subcutaneous 15 infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Therapeutics can be administered orally, rectally, parenterally, intracistemally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or 20 transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

25 Therapeutics of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics are administered orally, rectally, parenterally, intracistemally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, 30 diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics include suitable polymeric materials (such as, for example, semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules), suitable hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, and sparingly soluble derivatives (such as, for example, a sparingly soluble salt).

- 5 Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman et al., *Biopolymers* 22:547-556 (1983)), poly (2-hydroxyethyl methacrylate) (Langer et al., *J. Biomed. Mater. Res.* 15:167-277 (1981), and Langer, *Chem. Tech.* 12:98-105 (1982)), ethylene vinyl acetate (Langer et al., *Id.*) or poly-D-(-)-3-hydroxybutyric acid (EP 133,988).

10 Sustained-release Therapeutics also include liposomally entrapped Therapeutics of the invention (see generally, Langer, *Science* 249:1527-1533 (1990); Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler 15 (eds.), Liss, New York, pp. 317 -327 and 353-365 (1989)). Liposomes containing the Therapeutic are prepared by methods known per se: DE 3,218,121; Epstein et al., *Proc. Natl. Acad. Sci. (USA)* 82:3688-3692 (1985); Hwang et al., *Proc. Natl. Acad. Sci.(USA)* 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, 20 the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal Therapeutic.

In yet an additional embodiment, the Therapeutics of the invention are delivered by way of a pump (see Langer, *supra*; Sefton, *CRC Crit. Ref. Biomed. Eng.* 14:201 (1987); 25 Buchwald et al., *Surgery* 88:507 (1980); Saudek et al., *N. Engl. J. Med.* 321:574 (1989)).

Other controlled release systems are discussed in the review-by Langer (*Science* 249:1527-1533 (1990)).

For parenteral administration, in one embodiment, the Therapeutic is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form 30 (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e.. one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not

include oxidizing agents and other compounds that are known to be deleterious to the Therapeutic.

Generally, the formulations are prepared by contacting the Therapeutic uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the 5 product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that 10 enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic 15 polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

20 The Therapeutic is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any pharmaceutical used for therapeutic administration can be sterile. Sterility is 25 readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutics generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Therapeutics ordinarily will be stored in unit or multi-dose containers, for example, 30 sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous Therapeutic solution, and the resulting mixture is

lyophilized. The infusion solution is prepared by reconstituting the lyophilized Therapeutic using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the Therapeutics of the invention.

5 Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the Therapeutics may be employed in conjunction with other therapeutic compounds.

10 The Therapeutics of the invention may be administered alone or in combination with adjuvants. Adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to, alum, alum plus deoxycholate (ImmunoAg), MTP-PE (Biocine Corp.), QS21 (Genentech, Inc.), BCG, and MPL. In a specific embodiment, Therapeutics of the invention are administered in combination with alum. In another specific
15 embodiment, Therapeutics of the invention are administered in combination with QS-21. Further adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to, Monophosphoryl lipid immunomodulator, AdjuVax 100a, QS-21, QS-18, CRL1005, Aluminum salts, MF-59, and Virosomal adjuvant technology. Vaccines that may be administered with the Therapeutics of the invention include, but are not limited to,
20 vaccines directed toward protection against MMR (measles, mumps, rubella), polio, varicella, tetanus/diphtheria, hepatitis A, hepatitis B, haemophilus influenzae B, whooping cough, pneumonia, influenza, Lyme's Disease, rotavirus, cholera, yellow fever, Japanese encephalitis, poliomyelitis, rabies, typhoid fever, and pertussis. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or
25 concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

30 The Therapeutics of the invention may be administered alone or in combination with other therapeutic agents. Therapeutic agents that may be administered in combination with the Therapeutics of the invention, include but not limited to, other members of the TNF

family, chemotherapeutic agents, antibiotics, steroidal and non-steroidal anti-inflammatories, conventional immunotherapeutic agents, cytokines and/or growth factors. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are

5 administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

In one embodiment, the Therapeutics of the invention are administered in

10 combination with members of the TNF family. TNF, TNF-related or TNF-like molecules that may be administered with the Therapeutics of the invention include, but are not limited to, soluble forms of TNF-alpha, lymphotoxin-alpha (LT-alpha, also known as TNF-beta), LT-beta (found in complex heterotrimer LT-alpha2-beta), OPGL, FasL, CD27L, CD30L, CD40L, 4-1BBL, DcR3, OX40L, TNF-gamma (International Publication No. WO 15 96/14328), AIM-I (International Publication No. WO 97/33899), endokine-alpha (International Publication No. WO 98/07880), TR6 (International Publication No. WO 98/30694), OPG, and neutrokinin-alpha (International Publication No. WO 98/18921, OX40, and nerve growth factor (NGF), and soluble forms of Fas, CD30, CD27, CD40 and 4-IBB, TR2 (International Publication No. WO 96/34095), DR3 (International Publication No. WO 20 97/33904), DR4 (International Publication No. WO 98/32856), TR5 (International Publication No. WO 98/30693), TR6 (International Publication No. WO 98/30694), TR7 (International Publication No. WO 98/41629), TRANK, TR9 (International Publication No. WO 98/56892), TR10 (International Publication No. WO 98/54202), 312C2 (International Publication No. WO 98/06842), and TR12, and soluble forms CD154, CD70, and CD153.

25 In certain embodiments, Therapeutics of the invention are administered in combination with antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors. Nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, RETROVIR™ (zidovudine/AZT), VIDEX™ (didanosine/ddI), HIVID™ (zalcitabine/ddC), ZERIT™ (stavudine/d4T), EPIVIR™ (lamivudine/3TC), and COMBIVIR™ (zidovudine/lamivudine). Non-nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the

invention. include, but are not limited to, VIRAMUNE™ (nevirapine), REScriptor™ (delavirdine), and SUSTIVA™ (efavirenz). Protease inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, CRIXIVAN™ (indinavir), NORVIR™ (ritonavir), INVIRASE™ (saquinavir), and 5 VIRACEPT™ (nelfinavir). In a specific embodiment, antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors may be used in any combination with Therapeutics of the invention to treat AIDS and/or to prevent or treat HIV infection.

In other embodiments, Therapeutics of the invention may be administered in 10 combination with anti-opportunistic infection agents. Anti-opportunistic agents that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, TRIMETHOPRIM-SULFAMETHOXAZOLE™, DAPSONE™, PENTAMIDINE™, ATOVAQUONE™, ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, ETHAMBUTOL™, RIFABUTIN™, CLARITHROMYCIN™, AZITHROMYCIN™, 15 GANCICLOVIR™, FOSCARNET™, CIDOFOVIR™, FLUCONAZOLE™, ITRACONAZOLE™, KETOCONAZOLE™, ACYCLOVIR™, FAMCICOLVIR™, PYRIMETHAMINE™, LEUCOVORIN™, NEUPOGEN™ (filgrastim/G-CSF), and LEUKINE™ (sargramostim/GM-CSF). In a specific embodiment, Therapeutics of the invention are used in any combination with TRIMETHOPRIM-SULFAMETHOXAZOLE™, 20 DAPSONE™, PENTAMIDINE™, and/or ATOVAQUONE™ to prophylactically treat or prevent an opportunistic *Pneumocystis carinii* pneumonia infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, and/or ETHAMBUTOL™ to prophylactically treat or prevent an opportunistic *Mycobacterium avium* complex infection. In another specific 25 embodiment, Therapeutics of the invention are used in any combination with RIFABUTIN™, CLARITHROMYCIN™, and/or AZITHROMYCIN™ to prophylactically treat or prevent an opportunistic *Mycobacterium tuberculosis* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with GANCICLOVIR™, FOSCARNET™, and/or CIDOFOVIR™ to prophylactically treat or prevent an opportunistic 30 cytomegalovirus infection. In another specific embodiment, Therapeutics of the invention are used in any combination with FLUCONAZOLE™, ITRACONAZOLE™, and/or

- KETOCONAZOLE™ to prophylactically treat or prevent an opportunistic fungal infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ACYCLOVIR™ and/or FAMCICOLVIR™ to prophylactically treat or prevent an opportunistic herpes simplex virus type I and/or type II infection. In another specific embodiment, Therapeutics of the invention are used in any combination with PYRIMETHAMINE™ and/or LEUCOVORIN™ to prophylactically treat or prevent an opportunistic *Toxoplasma gondii* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with LEUCOVORIN™ and/or NEUPOGEN™ to prophylactically treat or prevent an opportunistic bacterial infection.
- In a further embodiment, the Therapeutics of the invention are administered in combination with an antiviral agent. Antiviral agents that may be administered with the Therapeutics of the invention include, but are not limited to, acyclovir, ribavirin, amantadine, and remantidine.
- In a further embodiment, the Therapeutics of the invention are administered in combination with an antibiotic agent. Antibiotic agents that may be administered with the Therapeutics of the invention include, but are not limited to, amoxicillin, beta-lactamases, aminoglycosides, beta-lactam (glycopeptide), beta-lactamases, Clindamycin, chloramphenicol, cephalosporins, ciprofloxacin, ciprofloxacin, erythromycin, fluoroquinolones, macrolides, metronidazole, penicillins, quinolones, rifampin, streptomycin, sulfonamide, tetracyclines, trimethoprim, trimethoprim-sulfamthoxazole, and vancomycin.
- Conventional nonspecific immunosuppressive agents, that may be administered in combination with the Therapeutics of the invention include, but are not limited to, steroids, cyclosporine, cyclosporine analogs, cyclophosphamide methylprednisolone, prednisone, azathioprine, FK-506, 15-deoxyspergualin, and other immunosuppressive agents that act by suppressing the function of responding T cells.
- In specific embodiments, Therapeutics of the invention are administered in combination with immunosuppressants. Immunosuppressants preparations that may be administered with the Therapeutics of the invention include, but are not limited to, ORTHOCLONE™ (OKT3), SANDIMMUNE™/NEORAL™/SANGDYA™ (cyclosporin), PROGRAF™ (tacrolimus), CELLCEPT™ (mycophenolate), Azathioprine, glucorticosteroids, and RAPAMUNE™ (sirolimus). In a specific embodiment, immunosuppressants may be

used to prevent rejection of organ or bone marrow transplantation.

In an additional embodiment, Therapeutics of the invention are administered alone or in combination with one or more intravenous immune globulin preparations. Intravenous immune globulin preparations that may be administered with the Therapeutics of the invention include, but not limited to, GAMMAR™, IVEEGAM™, SANDOGLOBULIN™, GAMMAGARD S/D™, and GAMIMUNE™. In a specific embodiment, Therapeutics of the invention are administered in combination with intravenous immune globulin preparations in transplantation therapy (e.g., bone marrow transplant).

In an additional embodiment, the Therapeutics of the invention are administered alone or in combination with an anti-inflammatory agent. Anti-inflammatory agents that may be administered with the Therapeutics of the invention include, but are not limited to, glucocorticoids and the nonsteroidal anti-inflammatories, aminoarylcarboxylic acid derivatives, arylacetic acid derivatives, arylbutyric acid derivatives, arylcarboxylic acids, arylpropionic acid derivatives, pyrazoles, pyrazolones, salicylic acid derivatives, thiazinecarboxamides, e-acetamidocaproic acid, S-adenosylmethionine, 3-amino-4-hydroxybutyric acid, amixetrine, bendazac, benzydamine, bucolome, difenpiramide, ditazol, emorfazole, guaiazulene, nabumetone, nimesulide, orgotein, oxaceprol, paranyline, perisoxal, pifoxime, proquazone, proxazole, and tenidap.

In another embodiment, compositions of the invention are administered in combination with a chemotherapeutic agent. Chemotherapeutic agents that may be administered with the Therapeutics of the invention include, but are not limited to, antibiotic derivatives (e.g., doxorubicin, bleomycin, daunorubicin, and dactinomycin); antiestrogens (e.g., tamoxifen); antimetabolites (e.g., fluorouracil, 5-FU, methotrexate, floxuridine, interferon alpha-2b, glutamic acid, plicamycin, mercaptoperine, and 6-thioguanine); cytotoxic agents (e.g., carmustine, BCNU, lomustine, CCNU, cytosine arabinoside, cyclophosphamide, estramustine, hydroxyurea, procarbazine, mitomycin, busulfan, cis-platin, and vincristine sulfate); hormones (e.g., medroxyprogesterone, estramustine phosphate sodium, ethinyl estradiol, estradiol, megestrol acetate, methyltestosterone, diethylstilbestrol diphosphate, chlorotrianisene, and testolactone); nitrogen mustard derivatives (e.g., mephalen, chorambucil, mechlorethamine (nitrogen mustard) and thiotapec); steroids and combinations (e.g., bethamethasone sodium phosphate); and others (e.g., dicarbazine, asparaginase, mitotane, vincristine sulfate, vinblastine sulfate, and etoposide).

- In a specific embodiment, Therapeutics of the invention are administered in combination with CHOP (cyclophosphamide, doxorubicin, vincristine, and prednisone) or any combination of the components of CHOP. In another embodiment, Therapeutics of the invention are administered in combination with Rituximab. In a further embodiment,
- 5 Therapeutics of the invention are administered with Rituxmab and CHOP, or Rituxmab and any combination of the components of CHOP.

10 In an additional embodiment, the Therapeutics of the invention are administered in combination with cytokines. Cytokines that may be administered with the Therapeutics of the invention include, but are not limited to, IL2, IL3, IL4, IL5, IL6, IL7, IL10, IL12, IL13, IL15, anti-CD40, CD40L, IFN-gamma and TNF-alpha. In another embodiment, Therapeutics of the invention may be administered with any interleukin, including, but not limited to, IL-1alpha, IL-1beta, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, and IL-21.

15 In an additional embodiment, the Therapeutics of the invention are administered in combination with angiogenic proteins. Angiogenic proteins that may be administered with the Therapeutics of the invention include, but are not limited to, Glioma Derived Growth Factor (GDF), as disclosed in European Patent Number EP-399816; Platelet Derived Growth Factor-A (PDGF-A), as disclosed in European Patent Number EP-682110; Platelet Derived Growth Factor-B (PDGF-B), as disclosed in European Patent Number EP-282317;

20 Placental Growth Factor (PIGF), as disclosed in International Publication Number WO 92/06194; Placental Growth Factor-2 (PIGF-2), as disclosed in Hauser et al., Gorwth Factors, 4:259-268 (1993); Vascular Endothelial Growth Factor (VEGF), as disclosed in International Publication Number WO 90/13649; Vascular Endothelial Growth Factor-A (VEGF-A), as disclosed in European Patent Number EP-506477; Vascular Endothelial Growth Factor-2

25 (VEGF-2), as disclosed in International Publication Number WO 96/39515; Vascular Endothelial Growth Factor B (VEGF-3); Vascular Endothelial Growth Factor B-186 (VEGF-B186), as disclosed in International Publication Number WO 96/26736; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/02543; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International

30 Publication Number WO 98/07832; and Vascular Endothelial Growth Factor-E (VEGF-E), as disclosed in German Patent Number DE19639601. The above mentioned references are incorporated herein by reference herein.

In an additional embodiment, the Therapeutics of the invention are administered in combination with hematopoietic growth factors. Hematopoietic growth factors that may be administered with the Therapeutics of the invention include, but are not limited to, LEUKINE™ (SARGRAMOSTIM™) and NEUPOGEN™ (FILGRASTIM™).

5 In an additional embodiment, the Therapeutics of the invention are administered in combination with Fibroblast Growth Factors. Fibroblast Growth Factors that may be administered with the Therapeutics of the invention include, but are not limited to, FGF-1, FGF-2, FGF-3, FGF-4, FGF-5, FGF-6, FGF-7, FGF-8, FGF-9, FGF-10, FGF-11, FGF-12, FGF-13, FGF-14, and FGF-15.

10 In additional embodiments, the Therapeutics of the invention are administered in combination with other therapeutic or prophylactic regimens, such as, for example, radiation therapy.

Example 14: Method of Treating Decreased Levels of the Polypeptide

15 The present invention relates to a method for treating an individual in need of an increased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an agonist of the invention (including polypeptides of the invention). Moreover, it will be appreciated that conditions caused by a decrease in the standard or normal expression level of a polypeptide of the present invention in an individual can be treated by administering the agonist or antagonist of the present invention. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a Therapeutic comprising an amount of the agonist or 20 antagonist to increase the activity level of the polypeptide in such an individual.

25

For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the agonist or antagonist for six consecutive days. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 13.

30 *Example 15: Method of Treating Increased Levels of the Polypeptide*

The present invention also relates to a method of treating an individual in need of a

decreased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an antagonist of the invention (including polypeptides and antibodies of the invention).

- In one example, antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, due to a variety of etiologies, such as cancer.
- For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 13.

Example 16: Method of Treatment Using Gene Therapy-Ex Vivo

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37 degree C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1 using primers and having appropriate restriction sites and initiation/stop codons, if

necessary. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene-of-interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytadex 3 microcarrier beads.

Example 17: Gene Therapy Using Endogenous Genes Corresponding To Polynucleotides of the Invention

Another method of gene therapy according to the present invention involves operably associating the endogenous polynucleotide sequence of the invention with a promoter via homologous recombination as described, for example, in U.S. Patent NO: 5,641,670, issued

June 24, 1997; International Publication NO: WO 96/29411, published September 26, 1996; International Publication NO: WO 94/12650, published August 4, 1994; Koller et al., *Proc. Natl. Acad. Sci. USA*, 86:8932-8935 (1989); and Zijlstra et al., *Nature*, 342:435-438 (1989). This method involves the activation of a gene which is present in the target cells, but which is
5 not expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made which contain a promoter and targeting sequences, which are homologous to the 5' non-coding sequence of endogenous polynucleotide sequence, flanking the promoter. The targeting sequence will be sufficiently near the 5' end of the polynucleotide sequence so the promoter will be operably linked to the
10 endogenous sequence upon homologous recombination. The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end
15 of the amplified promoter.

The amplified promoter and the amplified targeting sequences are digested with the appropriate restriction enzymes and subsequently treated with calf intestinal phosphatase. The digested promoter and digested targeting sequences are added together in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for
20 ligation of the two fragments. The construct is size fractionated on an agarose gel then purified by phenol extraction and ethanol precipitation.

In this Example, the polynucleotide constructs are administered as naked polynucleotides via electroporation. However, the polynucleotide constructs may also be administered with transfection-facilitating agents, such as liposomes, viral sequences, viral
25 particles, precipitating agents, etc. Such methods of delivery are known in the art.

Once the cells are transfected, homologous recombination will take place which results in the promoter being operably linked to the endogenous polynucleotide sequence. This results in the expression of polynucleotide corresponding to the polynucleotide in the cell. Expression may be detected by immunological staining, or any other method known in
30 the art.

Fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in DMEM + 10% fetal calf serum. Exponentially growing or early stationary phase

fibroblasts are trypsinized and rinsed from the plastic surface with nutrient medium. An aliquot of the cell suspension is removed for counting, and the remaining cells are subjected to centrifugation. The supernatant is aspirated and the pellet is resuspended in 5 ml of electroporation buffer (20 mM HEPES pH 7.3, 137 mM NaCl, 5 mM KCl, 0.7 mM Na₂HPO₄, 6 mM dextrose). The cells are re-centrifuged, the supernatant aspirated, and the cells resuspended in electroporation buffer containing 1 mg/ml acetylated bovine serum albumin. The final cell suspension contains approximately 3X10⁶ cells/ml. Electroporation should be performed immediately following resuspension.

Plasmid DNA is prepared according to standard techniques. For example, to construct a plasmid for targeting to the locus corresponding to the polynucleotide of the invention, plasmid pUC18 (MBI Fermentas, Amherst, NY) is digested with HindIII. The CMV promoter is amplified by PCR with an XbaI site on the 5' end and a BamHI site on the 3'end. Two non-coding sequences are amplified via PCR: one non-coding sequence (fragment 1) is amplified with a HindIII site at the 5' end and an XbaI site at the 3'end; the other non-coding sequence (fragment 2) is amplified with a BamHI site at the 5'end and a HindIII site at the 3'end. The CMV promoter and the fragments (1 and 2) are digested with the appropriate enzymes (CMV promoter - XbaI and BamHI; fragment 1 - XbaI; fragment 2 - BamHI) and ligated together. The resulting ligation product is digested with HindIII, and ligated with the HindIII-digested pUC18 plasmid.

Plasmid DNA is added to a sterile cuvette with a 0.4 cm electrode gap (Bio-Rad). The final DNA concentration is generally at least 120 µg/ml. 0.5 ml of the cell suspension (containing approximately 1.5.X10⁶ cells) is then added to the cuvette, and the cell suspension and DNA solutions are gently mixed. Electroporation is performed with a Gene-Pulser apparatus (Bio-Rad). Capacitance and voltage are set at 960 µF and 250-300 V, respectively. As voltage increases, cell survival decreases, but the percentage of surviving cells that stably incorporate the introduced DNA into their genome increases dramatically. Given these parameters, a pulse time of approximately 14-20 mSec should be observed.

Electroporated cells are maintained at room temperature for approximately 5 min, and the contents of the cuvette are then gently removed with a sterile transfer pipette. The cells are added directly to 10 ml of prewarmed nutrient media (DMEM with 15% calf serum) in a 10 cm dish and incubated at 37 degree C. The following day, the media is aspirated and replaced with 10 ml of fresh media and incubated for a further 16-24 hours.

The engineered fibroblasts are then injected into the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads. The fibroblasts now produce the protein product. The fibroblasts can then be introduced into a patient as described above.

5 *Example 18: Method of Treatment Using Gene Therapy - In Vivo*

-----Another aspect of the present invention is using *in vivo* gene therapy methods to treat disorders, diseases and conditions. The gene therapy method relates to the introduction of naked nucleic acid (DNA, RNA, and antisense DNA or RNA) sequences into an animal to 10 increase or decrease the expression of the polypeptide. The polynucleotide of the present invention may be operatively linked to a promoter or any other genetic elements necessary for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques and methods are known in the art, see, for example, WO90/11092, WO98/11779; U.S. Patent NO. 5693622, 5705151, 5580859; Tabata et al., Cardiovasc. Res. 35(3):470-479 15 (1997); Chao et al., Pharmacol. Res. 35(6):517-522 (1997); Wolff, Neuromuscul. Disord. 7(5):314-318 (1997); Schwartz et al., Gene Ther. 3(5):405-411 (1996); Tsurumi et al., Circulation 94(12):3281-3290 (1996) (incorporated herein by reference).

20 The polynucleotide constructs may be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, intestine and the like). The polynucleotide constructs can be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

25 The term "naked" polynucleotide, DNA or RNA, refers to sequences that are free from any delivery vehicle that acts to assist, promote, or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotides of the present invention may also be delivered in liposome formulations (such as those taught in Felgner P.L. et al. (1995) Ann. NY Acad. Sci. 772:126-139 and Abdallah B. et al. (1995) Biol. Cell 85(1):1-7) which can be prepared by methods well known to those skilled in the art.

30 The polynucleotide vector constructs used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Any strong promoter known to those skilled in the art can be used for driving the expression of DNA. Unlike other gene therapies techniques, one major advantage

of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

- 5 The polynucleotide construct can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by
- 10 fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by
- 15 injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. *In vivo* muscle cells are particularly competent in their ability to take up and express polynucleotides.
- 20 For the naked polynucleotide injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 g/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration. The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked polynucleotide constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.
- 25 The dose response effects of injected polynucleotide in muscle *in vivo* is determined

as follows. Suitable template DNA for production of mRNA coding for polypeptide of the present invention is prepared in accordance with a standard recombinant DNA methodology. The template DNA, which may be either circular or linear, is either used as naked DNA or complexed with liposomes. The quadriceps muscles of mice are then injected with various 5 amounts of the template DNA.

Five to six week old female and male Balb/C mice are anesthetized by intraperitoneal injection with 0.3 ml of 2.5% Avertin. A 1.5 cm incision is made on the anterior thigh, and the quadriceps muscle is directly visualized. The template DNA is injected in 0.1 ml of carrier in a 1 cc syringe through a 27 gauge needle over one minute, approximately 0.5 cm 10 from the distal insertion site of the muscle into the knee and about 0.2 cm deep. A suture is placed over the injection site for future localization, and the skin is closed with stainless steel clips.

After an appropriate incubation time (e.g., 7 days) muscle extracts are prepared by excising the entire quadriceps. Every fifth 15 um cross-section of the individual quadriceps 15 muscles is histochemically stained for protein expression. A time course for protein expression may be done in a similar fashion except that quadriceps from different mice are harvested at different times. Persistence of DNA in muscle following injection may be determined by Southern blot analysis after preparing total cellular DNA and HIRT supernatants from injected and control mice. The results of the above experimentation in 20 mice can be used to extrapolate proper dosages and other treatment parameters in humans and other animals using naked DNA.

Example 19: Transgenic Animals

25 The polypeptides of the invention can also be expressed in transgenic animals. Animals of any species, including, but not limited to, mice, rats, rabbits, hamsters, guinea pigs, pigs, micro-pigs, goats, sheep, cows and non-human primates, e.g., baboons, monkeys, and chimpanzees may be used to generate transgenic animals. In a specific embodiment, techniques described herein or otherwise known in the art, are used to express polypeptides 30 of the invention in humans, as part of a gene therapy protocol.

Any technique known in the art may be used to introduce the transgene (i.e., polynucleotides of the invention) into animals to produce the founder lines of transgenic

animals. Such techniques include, but are not limited to, pronuclear microinjection (Paterson et al., *Appl. Microbiol. Biotechnol.* 40:691-698 (1994); Carver et al., *Biotechnology* (NY) 11:1263-1270 (1993); Wright et al., *Biotechnology* (NY) 9:830-834 (1991); and Hoppe et al., U.S. Pat. No. 4,873,191 (1989)); retrovirus mediated gene transfer into germ lines (Van der Putten et al., *Proc. Natl. Acad. Sci., USA* 82:6148-6152 (1985)), blastocysts or embryos; gene targeting in embryonic stem cells (Thompson et al., *Cell* 56:313-321 (1989)); electroporation of cells or embryos (Lo, 1983, *Mol Cell. Biol.* 3:1803-1814 (1983)); introduction of the polynucleotides of the invention using a gene gun (see, e.g., Ulmer et al., *Science* 259:1745 (1993)); introducing nucleic acid constructs into embryonic pluripotent stem cells and transferring the stem cells back into the blastocyst; and sperm-mediated gene transfer (Lavitrano et al., *Cell* 57:717-723 (1989); etc. For a review of such techniques, see Gordon, "Transgenic Animals," *Intl. Rev. Cytol.* 115:171-229 (1989), which is incorporated by reference herein in its entirety.

Any technique known in the art may be used to produce transgenic clones containing polynucleotides of the invention, for example, nuclear transfer into enucleated oocytes of nuclei from cultured embryonic, fetal, or adult cells induced to quiescence (Campell et al., *Nature* 380:64-66 (1996); Wilmut et al., *Nature* 385:810-813 (1997)).

The present invention provides for transgenic animals that carry the transgene in all their cells, as well as animals which carry the transgene in some, but not all their cells, i.e., mosaic animals or chimeric. The transgene may be integrated as a single transgene or as multiple copies such as in concatamers, e.g., head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko et al. (Lasko et al., *Proc. Natl. Acad. Sci. USA* 89:6232-6236 (1992)). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the polynucleotide transgene be integrated into the chromosomal site of the endogenous gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous gene are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of the endogenous gene. The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene in only that cell type, by following, for example,

the teaching of Gu et al. (Gu et al.. Science 265:103-106 (1994)). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant gene
5 may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to verify that integration of the transgene has taken place. The level of mRNA expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques which include, but are not limited to, Northern blot analysis of tissue samples obtained from the animal, *in situ*
10 hybridization analysis, and reverse transcriptase-PCR (rt-PCR). Samples of transgenic gene-expressing tissue may also be evaluated immunocytochemically or immunohistochemically using antibodies specific for the transgene product.

Once the founder animals are produced, they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding strategies
15 include, but are not limited to: outbreeding of founder animals with more than one integration site in order to establish separate lines; inbreeding of separate lines in order to produce compound transgenics that express the transgene at higher levels because of the effects of additive expression of each transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order to both augment
20 expression and eliminate the need for screening of animals by DNA analysis; crossing of separate homozygous lines to produce compound heterozygous or homozygous lines; and breeding to place the transgene on a distinct background that is appropriate for an experimental model of interest.

Transgenic animals of the invention have uses which include, but are not limited to,
25 animal model systems useful in elaborating the biological function of polypeptides of the present invention, studying conditions and/or disorders associated with aberrant expression, and in screening for compounds effective in ameliorating such conditions and/or disorders.

Example 20: Knock-Out Animals

30

Endogenous gene expression can also be reduced by inactivating or "knocking out" the gene and/or its promoter using targeted homologous recombination. (E.g., see Smithies

et al.. Nature 317:230-234 (1985); Thomas & Capecchi, Cell 51:503-512 (1987); Thompson et al., Cell 5:313-321 (1989); each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional polynucleotide of the invention (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous 5 polynucleotide sequence (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfet cells that express polypeptides of the invention *in vivo*. In another embodiment, techniques known in the art are used to generate knockouts in cells that contain, but do not express the gene of interest. Insertion of the DNA construct, via targeted homologous recombination, 10 results in inactivation of the targeted gene. Such approaches are particularly suited in research and agricultural fields where modifications to embryonic stem cells can be used to generate animal offspring with an inactive targeted gene (e.g., see Thomas & Capecchi 1987 and Thompson 1989, *supra*). However this approach can be routinely adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to 15 the required site *in vivo* using appropriate viral vectors that will be apparent to those of skill in the art.

In further embodiments of the invention, cells that are genetically engineered to express the polypeptides of the invention, or alternatively, that are genetically engineered not to express the polypeptides of the invention (e.g., knockouts) are administered to a patient *in vivo*. Such cells may be obtained from the patient (i.e., animal, including human) or an MHC compatible donor and can include, but are not limited to fibroblasts, bone marrow cells, 20 blood cells (e.g., lymphocytes), adipocytes, muscle cells, endothelial cells etc. The cells are genetically engineered *in vitro* using recombinant DNA techniques to introduce the coding sequence of polypeptides of the invention into the cells, or alternatively, to disrupt the coding 25 sequence and/or endogenous regulatory sequence associated with the polypeptides of the invention, e.g., by transduction (using viral vectors, and preferably vectors that integrate the transgene into the cell genome) or transfection procedures, including, but not limited to, the use of plasmids, cosmids, YACs, naked DNA, electroporation, liposomes, etc. The coding sequence of the polypeptides of the invention can be placed under the control of a strong 30 constitutive or inducible promoter or promoter/enhancer to achieve expression, and preferably secretion, of the polypeptides of the invention. The engineered cells which express and preferably secrete the polypeptides of the invention can be introduced into the

patient systemically, e.g., in the circulation, or intraperitoneally.

Alternatively, the cells can be incorporated into a matrix and implanted in the body, e.g., genetically engineered fibroblasts can be implanted as part of a skin graft; genetically engineered endothelial cells can be implanted as part of a lymphatic or vascular graft. (See, 5 for example, Anderson et al. U.S. Patent No. 5,399,349; and Mulligan & Wilson, U.S. Patent No. 5,460,959 each of which is incorporated by reference herein in its entirety).

When the cells to be administered are non-autologous or non-MHC compatible cells, they can be administered using well known techniques which prevent the development of a host immune response against the introduced cells. For example, the cells may be introduced 10 in an encapsulated form which, while allowing for an exchange of components with the immediate extracellular environment, does not allow the introduced cells to be recognized by the host immune system.

Transgenic and "knock-out" animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of 15 polypeptides of the present invention, studying conditions and/or disorders associated with aberrant expression, and in screening for compounds effective in ameliorating such conditions and/or disorders.

*Example 22: Assays Detecting Stimulation or Inhibition of B cell Proliferation and
20 Differentiation*

Generation of functional humoral immune responses requires both soluble and cognate signaling between B-lineage cells and their microenvironment. Signals may impart a positive stimulus that allows a B-lineage cell to continue its programmed development, or a 25 negative stimulus that instructs the cell to arrest its current developmental pathway. To date, numerous stimulatory and inhibitory signals have been found to influence B cell responsiveness including IL-2, IL-4, IL-5, IL-6, IL-7, IL10, IL-13, IL-14 and IL-15. Interestingly, these signals are by themselves weak effectors but can, in combination with various co-stimulatory proteins, induce activation, proliferation, differentiation, homing, 30 tolerance and death among B cell populations.

One of the best studied classes of B-cell co-stimulatory proteins is the TNF-superfamily. Within this family CD40, CD27, and CD30 along with their respective ligands

CD154, CD70, and CD153 have been found to regulate a variety of immune responses. Assays which allow for the detection and/or observation of the proliferation and differentiation of these B-cell populations and their precursors are valuable tools in determining the effects various proteins may have on these B-cell populations in terms of 5 proliferation and differentiation. Listed below are two assays designed to allow for the detection of the differentiation, proliferation, or inhibition of B-cell populations and their precursors.

In Vitro Assay- Agonists or antagonists of the invention can be assessed for its ability to induce activation, proliferation, differentiation or inhibition and/or death in B-cell 10 populations and their precursors. The activity of the agonists or antagonists of the invention on purified human tonsillar B cells, measured qualitatively over the dose range from 0.1 to 10,000 ng/mL. is assessed in a standard B-lymphocyte co-stimulation assay in which purified tonsillar B cells are cultured in the presence of either formalin-fixed *Staphylococcus aureus* Cowan I (SAC) or immobilized anti-human IgM antibody as the priming agent. Second 15 signals such as IL-2 and IL-15 synergize with SAC and IgM crosslinking to elicit B cell proliferation as measured by tritiated-thymidine incorporation. Novel synergizing agents can be readily identified using this assay. The assay involves isolating human tonsillar B cells by magnetic bead (MACS) depletion of CD3-positive cells. The resulting cell population is greater than 95% B cells as assessed by expression of CD45R(B220).

20 Various dilutions of each sample are placed into individual wells of a 96-well plate to which are added 10^5 B-cells suspended in culture medium (RPMI 1640 containing 10% FBS, 5×10^{-5} M 2ME, 100U/ml penicillin, 10ug/ml streptomycin, and 10^{-5} dilution of SAC) in a total volume of 150ul. Proliferation or inhibition is quantitated by a 20h pulse (1uCi/well) with ^{3}H -thymidine (6.7 Ci/mM) beginning 72h post factor addition. The positive and 25 negative controls are IL2 and medium respectively.

In Vivo Assay- BALB/c mice are injected (i.p.) twice per day with buffer only, or 2 mg/Kg of agonists or antagonists of the invention, or truncated forms thereof. Mice receive this treatment for 4 consecutive days, at which time they are sacrificed and various tissues and serum collected for analyses. Comparison of H&E sections from normal spleens and 30 spleens treated with agonists or antagonists of the invention identify the results of the activity of the agonists or antagonists on spleen cells, such as the diffusion of peri-arterial lymphatic sheaths, and/or significant increases in the nucleated cellularity of the red pulp regions, which

may indicate the activation of the differentiation and proliferation of B-cell populations. Immunohistochemical studies using a B cell marker, anti-CD45R(B220), are used to determine whether any physiological changes to splenic cells, such as splenic disorganization, are due to increased B-cell representation within loosely defined B-cell zones that infiltrate established T-cell regions.

Flow cytometric analyses of the spleens from mice treated with agonist or antagonist is used to indicate whether the agonists or antagonists specifically increases the proportion of ThB+, CD45R(B220) dull B cells over that which is observed in control mice. Likewise, a predicted consequence of increased mature B-cell representation in vivo is a relative increase in serum Ig titers. Accordingly, serum IgM and IgA levels are compared between buffer and agonists or antagonists-treated mice.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

15

Example 23: T Cell Proliferation Assay

A CD3-induced proliferation assay is performed on PBMCs and is measured by the uptake of ^3H -thymidine. The assay is performed as follows. Ninety-six well plates are 20 coated with 100 μl /well of mAb to CD3 (HIT3a, Pharmingen) or isotype-matched control mAb (B33.1) overnight at 4 degrees C (1 $\mu\text{g}/\text{ml}$ in .05M bicarbonate buffer, pH 9.5), then washed three times with PBS. PBMC are isolated by F/H gradient centrifugation from human peripheral blood and added to quadruplicate wells ($5 \times 10^4/\text{well}$) of mAb coated plates in RPMI containing 10% FCS and P/S in the presence of varying concentrations of agonists 25 or antagonists of the invention (total volume 200 μl). Relevant protein buffer and medium alone are controls. After 48 hr. culture at 37 degrees C, plates are spun for 2 min. at 1000 rpm and 100 μl of supernatant is removed and stored -20 degrees C for measurement of IL-2 (or other cytokines) if effect on proliferation is observed. Wells are supplemented with 100 μl of medium containing 0.5 uCi of ^3H -thymidine and cultured at 37 degrees C for 18-24 hr. 30 Wells are harvested and incorporation of ^3H -thymidine used as a measure of proliferation. Anti-CD3 alone is the positive control for proliferation. IL-2 (100 U/ml) is also used as a control which enhances proliferation. Control antibody which does not induce proliferation

of T cells is used as the negative controls for the effects of agonists or antagonists of the invention.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test
5 the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 24: Effect of Agonists or Antagonists of the Invention on the Expression of MHC Class II, Costimulatory and Adhesion Molecules and Cell Differentiation of Monocytes and Monocyte-Derived Human Dendritic Cells

10

Dendritic cells are generated by the expansion of proliferating precursors found in the peripheral blood: adherent PBMC or elutriated monocytic fractions are cultured for 7-10 days with GM-CSF (50 ng/ml) and IL-4 (20 ng/ml). These dendritic cells have the characteristic phenotype of immature cells (expression of CD1, CD80, CD86, CD40 and MHC class II antigens). Treatment with activating factors, such as TNF- α , causes a rapid change in surface phenotype (increased expression of MHC class I and II, costimulatory and adhesion molecules, downregulation of FC γ RII, upregulation of CD83). These changes correlate with increased antigen-presenting capacity and with functional maturation of the dendritic cells.
15

FACS analysis of surface antigens is performed as follows. Cells are treated 1-3 days
20 with increasing concentrations of agonist or antagonist of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degrees C. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

25

Effect on the production of cytokines. Cytokines generated by dendritic cells, in particular IL-12, are important in the initiation of T-cell dependent immune responses. IL-12 strongly influences the development of Th1 helper T-cell immune response, and induces cytotoxic T and NK cell function. An ELISA is used to measure the IL-12 release as follows. Dendritic cells (10^6 /ml) are treated with increasing concentrations of agonists or antagonists of the invention for 24 hours. LPS (100 ng/ml) is added to the cell culture as positive control. Supernatants from the cell cultures are then collected and analyzed for IL-12 content using
30

commercial ELISA kit (e.g., R & D Systems (Minneapolis, MN)). The standard protocols provided with the kits are used.

Effect on the expression of MHC Class II, costimulatory and adhesion molecules. Three major families of cell surface antigens can be identified on monocytes: adhesion molecules, molecules involved in antigen presentation, and Fc receptor. Modulation of the expression of MHC class II antigens and other costimulatory molecules, such as B7 and ICAM-1, may result in changes in the antigen presenting capacity of monocytes and ability to induce T cell activation. Increase expression of Fc receptors may correlate with improved monocyte cytotoxic activity, cytokine release and phagocytosis.

FACS analysis is used to examine the surface antigens as follows. Monocytes are treated 1-5 days with increasing concentrations of agonists or antagonists of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degreesC. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

Monocyte activation and/or increased survival. Assays for molecules that activate (or alternatively, inactivate) monocytes and/or increase monocyte survival (or alternatively, decrease monocyte survival) are known in the art and may routinely be applied to determine whether a molecule of the invention functions as an inhibitor or activator of monocytes. Agonists or antagonists of the invention can be screened using the three assays described below. For each of these assays, Peripheral blood mononuclear cells (PBMC) are purified from single donor leukopacks (American Red Cross, Baltimore, MD) by centrifugation through a Histopaque gradient (Sigma). Monocytes are isolated from PBMC by counterflow centrifugal elutriation.

Monocyte Survival Assay. Human peripheral blood monocytes progressively lose viability when cultured in absence of serum or other stimuli. Their death results from internally regulated process (apoptosis). Addition to the culture of activating factors, such as TNF-alpha dramatically improves cell survival and prevents DNA fragmentation. Propidium iodide (PI) staining is used to measure apoptosis as follows. Monocytes are cultured for 48 hours in

polypropylene tubes in serum-free medium (positive control), in the presence of 100 ng/ml TNF-alpha (negative control), and in the presence of varying concentrations of the compound to be tested. Cells are suspended at a concentration of 2×10^6 /ml in PBS containing PI at a final concentration of 5 μ g/ml, and then incubated at room temperature for 5 minutes before 5 FACS analysis. PI uptake has been demonstrated to correlate with DNA fragmentation in this experimental paradigm.

- Effect on cytokine release. An important function of monocytes/macrophages is their regulatory activity on other cellular populations of the immune system through the release of 10 cytokines after stimulation. An ELISA to measure cytokine release is performed as follows. Human monocytes are incubated at a density of 5×10^5 cells/ml with increasing concentrations of agonists or antagonists of the invention and under the same conditions, but in the absence of agonists or antagonists. For IL-12 production, the cells are primed overnight with IFN (100 U/ml) in presence of agonist or antagonist of the invention. LPS (10 ng/ml) is then added. Conditioned media are collected after 24h and kept frozen until use. Measurement of TNF-alpha, IL-10, MCP-1 and IL-8 is then performed using a commercially available ELISA kit (e. g, R & D Systems (Minneapolis, MN)) and applying the standard protocols provided with the kit.
- 20 Oxidative burst. Purified monocytes are plated in 96-w plate at $2-1 \times 10^5$ cell/well. Increasing concentrations of agonists or antagonists of the invention are added to the wells in a total volume of 0.2 ml culture medium (RPMI 1640 + 10% FCS, glutamine and antibiotics). After 3 days incubation, the plates are centrifuged and the medium is removed from the wells. To the macrophage monolayers, 0.2 ml per well of phenol red solution (140 mM NaCl, 10 mM 25 potassium phosphate buffer pH 7.0, 5.5 mM dextrose, 0.56 mM phenol red and 19 U/ml of HRPO) is added, together with the stimulant (200 nM PMA). The plates are incubated at 37°C for 2 hours and the reaction is stopped by adding 20 μ l 1N NaOH per well. The absorbance is read at 610 nm. To calculate the amount of H₂O₂ produced by the macrophages, a standard curve of a H₂O₂ solution of known molarity is performed for each 30 experiment.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test

the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 25: Biological Effects of Agonists or Antagonists of the Invention

5

Astrocyte and Neuronal Assays.

Agonists or antagonists of the invention, expressed in *Escherichia coli* and purified as described above, can be tested for activity in promoting the survival, neurite outgrowth, or phenotypic differentiation of cortical neuronal cells and for inducing the proliferation of glial fibrillary acidic protein immunopositive cells, astrocytes. The selection of cortical cells for the bioassay is based on the prevalent expression of FGF-1 and FGF-2 in cortical structures and on the previously reported enhancement of cortical neuronal survival resulting from FGF-2 treatment. A thymidine incorporation assay, for example, can be used to elucidate an agonist or antagonist of the invention's activity on these cells.

Moreover, previous reports describing the biological effects of FGF-2 (basic FGF) on cortical or hippocampal neurons *in vitro* have demonstrated increases in both neuron survival and neurite outgrowth (Walicke et al., "Fibroblast growth factor promotes survival of dissociated hippocampal neurons and enhances neurite extension." *Proc. Natl. Acad. Sci. USA* 83:3012-3016. (1986), assay herein incorporated by reference in its entirety). However, reports from experiments done on PC-12 cells suggest that these two responses are not necessarily synonymous and may depend on not only which FGF is being tested but also on which receptor(s) are expressed on the target cells. Using the primary cortical neuronal culture paradigm, the ability of an agonist or antagonist of the invention to induce neurite outgrowth can be compared to the response achieved with FGF-2 using, for example, a thymidine incorporation assay.

Fibroblast and endothelial cell assays.

Human lung fibroblasts are obtained from Clonetics (San Diego, CA) and maintained in growth media from Clonetics. Dermal microvascular endothelial cells are obtained from Cell Applications (San Diego, CA). For proliferation assays, the human lung fibroblasts and

dermal microvascular endothelial cells can be cultured at 5,000 cells/well in a 96-well plate for one day in growth medium. The cells are then incubated for one day in 0.1% BSA basal medium. After replacing the medium with fresh 0.1% BSA medium, the cells are incubated with the test proteins for 3 days. Alamar Blue (Alamar Biosciences, Sacramento, CA) is 5 added to each well to a final concentration of 10%. The cells are incubated for 4 hr. Cell viability is measured by reading in a CytoFluor fluorescence reader. For the PGE₂ assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or 10 agonists or antagonists of the invention with or without IL-1 α for 24 hours. The supernatants are collected and assayed for PGE₂ by EIA kit (Cayman, Ann Arbor, MI). For the IL-6 assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or with or without agonists or antagonists of the invention IL-1 α for 24 hours. The supernatants are collected and assayed for IL-6 by ELISA kit (Endogen, Cambridge, MA).

15 Human lung fibroblasts are cultured with FGF-2 or agonists or antagonists of the invention for 3 days in basal medium before the addition of Alamar Blue to assess effects on growth of the fibroblasts. FGF-2 should show a stimulation at 10 - 2500 ng/ml which can be used to compare stimulation with agonists or antagonists of the invention.

20 Parkinson Models.

The loss of motor function in Parkinson's disease is attributed to a deficiency of striatal dopamine resulting from the degeneration of the nigrostriatal dopaminergic projection neurons. An animal model for Parkinson's that has been extensively characterized involves the systemic administration of 1-methyl-4 phenyl 1,2,3,6-tetrahydropyridine (MPTP). In the 25 CNS, MPTP is taken-up by astrocytes and catabolized by monoamine oxidase B to 1-methyl-4-phenyl pyridine (MPP⁺) and released. Subsequently, MPP⁺ is actively accumulated in dopaminergic neurons by the high-affinity reuptake transporter for dopamine. MPP⁺ is then concentrated in mitochondria by the electrochemical gradient and selectively inhibits nicotidamide adenine disphosphate: ubiquinone oxidoreductionase (complex I), thereby 30 interfering with electron transport and eventually generating oxygen radicals.

It has been demonstrated in tissue culture paradigms that FGF-2 (basic FGF) has

trophic activity towards nigral dopaminergic neurons (Ferrari et al., Dev. Biol. 1989). Recently, Dr. Unsicker's group has demonstrated that administering FGF-2 in gel foam implants in the striatum results in the near complete protection of nigral dopaminergic neurons from the toxicity associated with MPTP exposure (Otto and Unsicker, J. 5 Neuroscience, 1990).

Based on the data with FGF-2, agonists or antagonists of the invention can be evaluated to determine whether it has an action similar to that of FGF-2 in enhancing dopaminergic neuronal survival *in vitro* and it can also be tested *in vivo* for protection of dopaminergic neurons in the striatum from the damage associated with MPTP treatment. The 10 potential effect of an agonist or antagonist of the invention is first examined *in vitro* in a dopaminergic neuronal cell culture paradigm. The cultures are prepared by dissecting the midbrain floor plate from gestation day 14 Wistar rat embryos. The tissue is dissociated with trypsin and seeded at a density of 200,000 cells/cm² on polyorthinine-laminin coated glass coverslips. The cells are maintained in Dulbecco's Modified Eagle's medium and F12 15 medium containing hormonal supplements (N1). The cultures are fixed with paraformaldehyde after 8 days *in vitro* and are processed for tyrosine hydroxylase, a specific marker for dopaminergic neurons, immunohistochemical staining. Dissociated cell cultures are prepared from embryonic rats. The culture medium is changed every third day and the factors are also added at that time.

20 Since the dopaminergic neurons are isolated from animals at gestation day 14, a developmental time which is past the stage when the dopaminergic precursor cells are proliferating, an increase in the number of tyrosine hydroxylase immunopositive neurons would represent an increase in the number of dopaminergic neurons surviving *in vitro*. Therefore, if an agonist or antagonist of the invention acts to prolong the survival of 25 dopaminergic neurons, it would suggest that the agonist or antagonist may be involved in Parkinson's Disease.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Vascular Endothelial Cells

On day 1, human umbilical vein endothelial cells (HUVEC) are seeded at 2.5×10^4 cells/35 mm dish density in M199 medium containing 4% fetal bovine serum (FBS), 16 units/ml heparin, and 50 units/ml endothelial cell growth supplements (ECGS, Biotechnology, Inc.). On day 2, the medium is replaced with M199 containing 10% FBS, 8 units/ml heparin. An agonist or antagonist of the invention, and positive controls, such as VEGF and basic FGF (bFGF) are added, at varying concentrations. On days 4 and 6, the medium is replaced. On day 8, cell number is determined with a Coulter Counter.

10 An increase in the number of HUVEC cells indicates that the compound of the invention may proliferate vascular endothelial cells, while a decrease in the number of HUVEC cell indicates that the compound of the invention inhibits vascular endothelial cells.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity 15 of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

Example 27: Rat Corneal Wound Healing Model

This animal model shows the effect of an agonist or antagonist of the invention on 20 neovascularization. The experimental protocol includes:

- a) Making a 1-1.5 mm long incision from the center of cornea into the stromal layer.
- b) Inserting a spatula below the lip of the incision facing the outer corner of the eye.
- c) Making a pocket (its base is 1-1.5 mm from the edge of the eye).
- d) Positioning a pellet, containing 50ng- 5ug of an agonist or antagonist of the invention, within the pocket.
- e) Treatment with an agonist or antagonist of the invention can also be applied topically to the corneal wounds in a dosage range of 20mg - 500mg (daily treatment for five days).

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test

the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 28: Diabetic Mouse and Glucocorticoid-Impaired Wound Healing Models

5 A. *Diabetic db+/db+ Mouse Model.*

To demonstrate that an agonist or antagonist of the invention accelerates the healing process, the genetically diabetic mouse model of wound healing is used. The full thickness wound healing model in the db+/db+ mouse is a well characterized, clinically relevant and reproducible model of impaired wound healing. Healing of the diabetic wound is dependent 10 on formation of granulation tissue and re-epithelialization rather than contraction (Gartner, M.H. *et al.*, *J. Surg. Res.* 52:389 (1992); Greenhalgh, D.G. *et al.*, *Am. J. Pathol.* 136:1235 (1990)).

The diabetic animals have many of the characteristic features observed in Type II diabetes mellitus. Homozygous (db+/db+) mice are obese in comparison to their normal 15 heterozygous (db+/+m) littermates. Mutant diabetic (db+/db+) mice have a single autosomal recessive mutation on chromosome 4 (db+) (Coleman *et al.* *Proc. Natl. Acad. Sci. USA* 77:283-293 (1982)). Animals show polyphagia, polydipsia and polyuria. Mutant diabetic mice (db+/db+) have elevated blood glucose, increased or normal insulin levels, and suppressed cell-mediated immunity (Mandel *et al.*, *J. Immunol.* 120:1375 (1978); Debray-Sachs, M. *et al.*, *Clin. Exp. Immunol.* 51(1):1-7 (1983); Leiter *et al.*, *Am. J. of Pathol.* 114:46-20 55 (1985)). Peripheral neuropathy, myocardial complications, and microvascular lesions, basement membrane thickening and glomerular filtration abnormalities have been described in these animals (Norido, F. *et al.*, *Exp. Neurol.* 83(2):221-232 (1984); Robertson *et al.*, *Diabetes* 29(1):60-67 (1980); Giacomelli *et al.*, *Lab Invest.* 40(4):460-473 (1979); Coleman, 25 D.L., *Diabetes* 31 (Suppl):1-6 (1982)). These homozygous diabetic mice develop hyperglycemia that is resistant to insulin analogous to human type II diabetes (Mandel *et al.*, *J. Immunol.* 120:1375-1377 (1978)).

The characteristics observed in these animals suggests that healing in this model may be similar to the healing observed in human diabetes (Greenhalgh, *et al.*, *Am. J. of Pathol.* 30 /36:1235-1246 (1990)).

Genetically diabetic female C57BL/KsJ (db+/db+) mice and their non-diabetic (db+/+m) heterozygous littermates are used in this study (Jackson Laboratories). The

animals are purchased at 6 weeks of age and are 8 weeks old at the beginning of the study. Animals are individually housed and received food and water ad libitum. All manipulations are performed using aseptic techniques. The experiments are conducted according to the rules and guidelines of Human Genome Sciences, Inc. Institutional Animal Care and Use

5 Committee and the Guidelines for the Care and Use of Laboratory Animals.

Wounding protocol is performed according to previously reported methods (Tsuboi, R. and Rifkin, D.B., *J. Exp. Med.* 172:245-251 (1990)). Briefly, on the day of wounding, animals are anesthetized with an intraperitoneal injection of Avertin (0.01 mg/mL), 2,2,2-tribromoethanol and 2-methyl-2-butanol dissolved in deionized water. The dorsal region of
10 the animal is shaved and the skin washed with 70% ethanol solution and iodine. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is then created using a Keyes tissue punch. Immediately following wounding, the surrounding skin is gently stretched to eliminate wound expansion. The wounds are left open for the duration of the experiment. Application of the treatment is given topically for 5 consecutive days
15 commencing on the day of wounding. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of surgery and at two day intervals thereafter. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically
20 using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

An agonist or antagonist of the invention is administered using at a range different doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

25 Animals are euthanized on day 8 with an intraperitoneal injection of sodium pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for histology and immunohistochemistry. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes between biopsy sponges for further processing.

Three groups of 10 animals each (5 diabetic and 5 non-diabetic controls) are evaluated: 1)
30 Vehicle placebo control, 2) untreated group, and 3) treated group.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis and obtaining the total square area of the wound. Contraction is then estimated by establishing

the differences between the initial wound area (day 0) and that of post treatment (day 8). The wound area on day 1 is 64mm², the corresponding size of the dermal punch. Calculations are made using the following formula:

$$5 \quad [Open\ area\ on\ day\ 8] - [Open\ area\ on\ day\ 1] / [Open\ area\ on\ day\ 1]$$

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned perpendicular to the wound surface (5mm) and cut using a Reichert-Jung microtome. Routine hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected 10 wounds. Histologic examination of the wounds are used to assess whether the healing process and the morphologic appearance of the repaired skin is altered by treatment with an agonist or antagonist of the invention. This assessment included verification of the presence of cell accumulation, inflammatory cells, capillaries, fibroblasts, re-epithelialization and epidermal maturity (Greenhalgh, D.G. *et al.*, *Am. J. Pathol.* 136:1235 (1990)). A calibrated 15 lens micrometer is used by a blinded observer.

Tissue sections are also stained immunohistochemically with a polyclonal rabbit anti-human keratin antibody using ABC Elite detection system. Human skin is used as a positive tissue control while non-immune IgG is used as a negative control. Keratinocyte growth is determined by evaluating the extent of reepithelialization of the wound using a calibrated 20 lens micrometer.

Proliferating cell nuclear antigen/cyclin (PCNA) in skin specimens is demonstrated by using anti-PCNA antibody (1:50) with an ABC Elite detection system. Human colon cancer served as a positive tissue control and human brain tissue is used as a negative tissue control. Each specimen included a section with omission of the primary antibody and 25 substitution with non-immune mouse IgG. Ranking of these sections is based on the extent of proliferation on a scale of 0-8, the lower side of the scale reflecting slight proliferation to the higher side reflecting intense proliferation.

Experimental data are analyzed using an unpaired t test. A p value of < 0.05 is considered significant.

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B. Steroid Impaired Rat Model

The inhibition of wound healing by steroids has been well documented in various *in vitro* and

in vivo systems (Wahl, Glucocorticoids and Wound healing. In: Anti-Inflammatory Steroid Action: Basic and Clinical Aspects. 280-302 (1989); Wahlet *et al.*, *J. Immunol.* 115: 476-481 (1975); Werb *et al.*, *J. Exp. Med.* 147:1684-1694 (1978)). Glucocorticoids retard wound healing by inhibiting angiogenesis, decreasing vascular permeability (Ebert *et al.*, *An. Intern. Med.* 37:701-705 (1952)), fibroblast proliferation, and collagen synthesis (Beck *et al.*, *Growth Factors.* 5: 295-304 (1991); Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978)) and producing a transient reduction of circulating monocytes (Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978); Wahl, "Glucocorticoids and wound healing", In: Antiinflammatory Steroid Action: Basic and Clinical Aspects, Academic Press, New York, pp. 280-302 (1989)). The systemic administration of steroids to impaired wound healing is a well establish phenomenon in rats (Beck *et al.*, *Growth Factors.* 5: 295-304 (1991); Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978); Wahl, "Glucocorticoids and wound healing", In: Antiinflammatory Steroid Action: Basic and Clinical Aspects, Academic Press, New York, pp. 280-302 (1989); Pierce *et al.*, *Proc. Natl. Acad. Sci. USA* 86: 2229-2233 (1989)).

To demonstrate that an agonist or antagonist of the invention can accelerate the healing process, the effects of multiple topical applications of the agonist or antagonist on full thickness excisional skin wounds in rats in which healing has been impaired by the systemic administration of methylprednisolone is assessed.

Young adult male Sprague Dawley rats weighing 250-300 g (Charles River Laboratories) are used in this example. The animals are purchased at 8 weeks of age and are 9 weeks old at the beginning of the study. The healing response of rats is impaired by the systemic administration of methylprednisolone (17mg/kg/rat intramuscularly) at the time of wounding. Animals are individually housed and received food and water *ad libitum*. All manipulations are performed using aseptic techniques. This study is conducted according to the rules and guidelines of Human Genome Sciences, Inc. Institutional Animal Care and Use Committee and the Guidelines for the Care and Use of Laboratory Animals.

The wounding protocol is followed according to section A, above. On the day of wounding, animals are anesthetized with an intramuscular injection of ketamine (50 mg/kg) and xylazine (5 mg/kg). The dorsal region of the animal is shaved and the skin washed with 70% ethanol and iodine solutions. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is created using a Keyes tissue punch. The wounds are left open for the duration of the experiment. Applications of the testing materials

are given topically once a day for 7 consecutive days commencing on the day of wounding and subsequent to methylprednisolone administration. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of
5 wounding and at the end of treatment. Wound closure is determined by daily measurement on
days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated
Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and
the wound is covered by a continuous epithelium.

The agonist or antagonist of the invention is administered using at a range different
10 doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups
received 50mL of vehicle solution.

Animals are euthanized on day 8 with an intraperitoneal injection of sodium
pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for
histology. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes
15 between biopsy sponges for further processing.

Four groups of 10 animals each (5 with methylprednisolone and 5 without
glucocorticoid) are evaluated: 1) Untreated group 2) Vehicle placebo control 3) treated
groups.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis
20 and obtaining the total area of the wound. Closure is then estimated by establishing the
differences between the initial wound area (day 0) and that of post treatment (day 8). The
wound area on day 1 is 64mm², the corresponding size of the dermal punch. Calculations
are made using the following formula:

$$25 \quad [\text{Open area on day 8}] - [\text{Open area on day 1}] / [\text{Open area on day 1}]$$

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned
perpendicular to the wound surface (5mm) and cut using an Olympus microtome. Routine
hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected wounds.
30 Histologic examination of the wounds allows assessment of whether the healing process and
the morphologic appearance of the repaired skin is improved by treatment with an agonist or
antagonist of the invention. A calibrated lens micrometer is used by a blinded observer to

determine the distance of the wound gap.

Experimental data are analyzed using an unpaired t test. A p value of < 0.05 is considered significant.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 29: Lymphadema Animal Model

10 The purpose of this experimental approach is to create an appropriate and consistent lymphedema model for testing the therapeutic effects of an agonist or antagonist of the invention in lymphangiogenesis and re-establishment of the lymphatic circulatory system in the rat hind limb. Effectiveness is measured by swelling volume of the affected limb, quantification of the amount of lymphatic vasculature, total blood plasma protein, and
15 histopathology. Acute lymphedema is observed for 7-10 days. Perhaps more importantly, the chronic progress of the edema is followed for up to 3-4 weeks.

Prior to beginning surgery, blood sample is drawn for protein concentration analysis. Male rats weighing approximately ~350g are dosed with Pentobarbital. Subsequently, the right legs are shaved from knee to hip. The shaved area is swabbed with gauze soaked in
20 70% EtOH. Blood is drawn for serum total protein testing. Circumference and volumetric measurements are made prior to injecting dye into paws after marking 2 measurement levels (0.5 cm above heel, at mid-pt of dorsal paw). The intradermal dorsum of both right and left paws are injected with 0.05 ml of 1% Evan's Blue. Circumference and volumetric measurements are then made following injection of dye into paws.

25 Using the knee joint as a landmark, a mid-leg inguinal incision is made circumferentially allowing the femoral vessels to be located. Forceps and hemostats are used to dissect and separate the skin flaps. After locating the femoral vessels, the lymphatic vessel that runs along side and underneath the vessel(s) is located. The main lymphatic vessels in this area are then electrically coagulated or suture ligated.

30 Using a microscope, muscles in back of the leg (near the semitendinosus and adductors) are bluntly dissected. The popliteal lymph node is then located. The 2 proximal and 2 distal lymphatic vessels and distal blood supply of the popliteal node are then and

ligated by suturing. The popliteal lymph node, and any accompanying adipose tissue, is then removed by cutting connective tissues.

Care is taken to control any mild bleeding resulting from this procedure. After lymphatics are occluded, the skin flaps are sealed by using liquid skin (Vetbond) (AJ Buck).

- 5 The separated skin edges are sealed to the underlying muscle tissue while leaving a gap of ~0.5 cm around the leg. Skin also may be anchored by suturing to underlying muscle when necessary.

- To avoid infection, animals are housed individually with mesh (no bedding). Recovering animals are checked daily through the optimal edematous peak, which typically occurred by day 5-7. The plateau edematous peak are then observed. To evaluate the intensity of the lymphedema, the circumference and volumes of 2 designated places on each paw before operation and daily for 7 days are measured. The effect plasma proteins on lymphedema is determined and whether protein analysis is a useful testing perimeter is also investigated. The weights of both control and edematous limbs are evaluated at 2 places.
- 15 Analysis is performed in a blind manner.

Circumference Measurements: Under brief gas anesthetic to prevent limb movement, a cloth tape is used to measure limb circumference. Measurements are done at the ankle bone and dorsal paw by 2 different people then those 2 readings are averaged. Readings are taken from both control and edematous limbs.

- 20 Volumetric Measurements: On the day of surgery, animals are anesthetized with Pentobarbital and are tested prior to surgery. For daily volumetrics animals are under brief halothane anesthetic (rapid immobilization and quick recovery), both legs are shaved and equally marked using waterproof marker on legs. Legs are first dipped in water, then dipped into instrument to each marked level then measured by Buxco edema software(Chen/Victor).
- 25 Data is recorded by one person, while the other is dipping the limb to marked area.

Blood-plasma protein measurements: Blood is drawn, spun, and serum separated prior to surgery and then at conclusion for total protein and Ca²⁺ comparison.

- 30 Limb Weight Comparison: After drawing blood, the animal is prepared for tissue collection. The limbs are amputated using a quillitine, then both experimental and control legs are cut at the ligature and weighed. A second weighing is done as the tibio-cacaneal joint is disarticulated and the foot is weighed.

Histological Preparations: The transverse muscle located behind the knee (popliteal)

area is dissected and arranged in a metal mold, filled with freezeGel, dipped into cold methylbutane, placed into labeled sample bags at - 80EC until sectioning. Upon sectioning, the muscle is observed under fluorescent microscopy for lymphatics..

5 The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 30: Suppression of TNF alpha-induced adhesion molecule expression by a Agonist or Antagonist of the Invention

10

The recruitment of lymphocytes to areas of inflammation and angiogenesis involves specific receptor-ligand interactions between cell surface adhesion molecules (CAMs) on lymphocytes and the vascular endothelium. The adhesion process, in both normal and pathological settings, follows a multi-step cascade that involves intercellular adhesion 15 molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), and endothelial leukocyte adhesion molecule-1 (E-selectin) expression on endothelial cells (EC). The expression of these molecules and others on the vascular endothelium determines the efficiency with which leukocytes may adhere to the local vasculature and extravasate into the local tissue during the development of an inflammatory response. The local concentration of 20 cytokines and growth factor participate in the modulation of the expression of these CAMs.

Tumor necrosis factor alpha (TNF-a), a potent proinflammatory cytokine, is a stimulator of all three CAMs on endothelial cells and may be involved in a wide variety of inflammatory responses, often resulting in a pathological outcome.

25 The potential of an agonist or antagonist of the invention to mediate a suppression of TNF-a induced CAM expression can be examined. A modified ELISA assay which uses ECs as a solid phase absorbent is employed to measure the amount of CAM expression on TNF-a treated ECs when co-stimulated with a member of the FGF family of proteins.

To perform the experiment, human umbilical vein endothelial cell (HUVEC) cultures 30 are obtained from pooled cord harvests and maintained in growth medium (EGM-2; Clonetics, San Diego, CA) supplemented with 10% FCS and 1% penicillin/streptomycin in a 37 degree C humidified incubator containing 5% CO₂. HUVECs are seeded in 96-well plates at concentrations of 1 x 10⁴ cells/well in EGM medium at 37 degree C for 18-24 hrs or

until confluent. The monolayers are subsequently washed 3 times with a serum-free solution of RPMI-1640 supplemented with 100 U/ml penicillin and 100 mg/ml streptomycin, and treated with a given cytokine and/or growth factor(s) for 24 h at 37 degree C. Following incubation. the cells are then evaluated for CAM expression.

5 Human Umbilical Vein Endothelial cells (HUVECs) are grown in a standard 96 well plate to confluence. Growth medium is removed from the cells and replaced with 90 ul of 199 Medium (10% FBS). Samples for testing and positive or negative controls are added to the plate in triplicate (in 10 ul volumes). Plates are incubated at 37 degree C for either 5 h (selectin and integrin expression) or 24 h (integrin expression only). Plates are aspirated to
10 remove medium and 100 μ l of 0.1% paraformaldehyde-PBS(with Ca⁺⁺ and Mg⁺⁺) is added to each well. Plates are held at 4°C for 30 min.

Fixative is then removed from the wells and wells are washed 1X with PBS(+Ca,Mg)+0.5% BSA and drained. Do not allow the wells to dry. Add 10 μ l of diluted primary antibody to the test and control wells. Anti-ICAM-1-Biotin, Anti-VCAM-1-Biotin
15 and Anti-E-selectin-Biotin are used at a concentration of 10 μ g/ml (1:10 dilution of 0.1 mg/ml stock antibody). Cells are incubated at 37°C for 30 min. in a humidified environment. Wells are washed X3 with PBS(+Ca,Mg)+0.5% BSA.

Then add 20 μ l of diluted ExtrAvidin-Alkaline Phosphotase (1:5,000 dilution) to each well and incubated at 37°C for 30 min. Wells are washed X3 with PBS(+Ca,Mg)+0.5%
20 BSA. 1 tablet of p-Nitrophenol Phosphate pNPP is dissolved in 5 ml of glycine buffer (pH 10.4). 100 μ l of pNPP substrate in glycine buffer is added to each test well. Standard wells in triplicate are prepared from the working dilution of the ExtrAvidin-Alkaline Phosphotase in glycine buffer: 1:5,000 (10^0) > $10^{-0.5}$ > 10^{-1} > $10^{-1.5}$. 5 μ l of each dilution is added to triplicate wells and the resulting AP content in each well is 5.50 ng, 1.74 ng, 0.55 ng, 0.18 ng. 100 μ l
25 of pNNP reagent must then be added to each of the standard wells. The plate must be incubated at 37°C for 4h. A volume of 50 μ l of 3M NaOH is added to all wells. The results are quantified on a plate reader at 405 nm. The background subtraction option is used on blank wells filled with glycine buffer only. The template is set up to indicate the concentration of AP-conjugate in each standard well [5.50 ng; 1.74 ng; 0.55 ng; 0.18 ng].
30 Results are indicated as amount of bound AP-conjugate in each sample.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test

the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 31: Production Of Polypeptide of the Invention For High-Throughput Screening Assays

5

The following protocol produces a supernatant containing polypeptide of the present invention to be tested. This supernatant can then be used in the Screening Assays described in Examples 33-42.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml
10 in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working
solution of 50 μ g/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at
RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel
pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine
15 solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the
well until just prior to plating the cells and plates may be poly-lysine coated in advance for
up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml
DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-
604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E
20 Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-
012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small
volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing
a polynucleotide insert, produced by the methods described in Examples 8-10, into an
25 appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of
the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix.
Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add
150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert
should be transfected with each set of transfections.

30 Preferably, the transfection should be performed by tag-teaming the following tasks.
By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on
PBS. First, person A aspirates off the media from four 24-well plates of cells, and then

person B rinses each well with .5-1ml PBS. Person A then aspirates off PBS rinse, and person B, using a12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37 degree C for 6 hours.

- 5 While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or HGS CHO-5 media (116.6 mg/L of CaCl₂ (anhyd); 0.00130 mg/L CuSO₄·5H₂O; 0.050 mg/L of Fe(NO₃)₃·9H₂O; 0.417 mg/L of FeSO₄·7H₂O; 311.80 mg/L of Kcl; 28.64 mg/L of MgCl₂; 48.84 mg/L of MgSO₄; 6995.50 mg/L of NaCl; 2400.0 mg/L of NaHCO₃; 62.50 mg/L of NaH₂PO₄·H₂O; 71.02 mg/L of Na₂HPO₄; .4320 mg/L of ZnSO₄·7H₂O; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitric Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H₂O; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H₂O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H₂O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 20.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na-2H₂O; and 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; 0.680 mg/L of Vitamin B₁₂; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine; 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal Acetate. Adjust

osmolarity to 327 mOsm) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

- The transfection reaction is terminated, preferably by tag-teaming, at the end of the
5 incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37 degree C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

- On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well
10 can then be used in the assays described in Examples 33-40.

- It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide of the present invention directly (e.g., as a secreted protein) or by polypeptide of the present invention inducing expression of other proteins, which are then secreted into the supernatant.
15 Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

Example 32: Construction of GAS Reporter Construct

- 20 One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

- 25 GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called
30 mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon

tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

5 The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN- α , IFN- γ ,
10 and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:1548)).

15 Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter
20 molecules, activators of the Jaks-STATs pathway can be identified.

<u>Ligand</u>	<u>JAKs</u>				<u>STATS GAS(elements) or ISRE</u>	
	<u>tyk2</u>	<u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>		

IFN family

5	IFN- α /B	+	+	-	-	1,2,3	ISRE
	IFN- γ		+	+	-	1	GAS
	(IRF1>Lys6>IFP)						
	IL-10		+	?	?	-	1,3

gp130 family

10	IL-6 (Pleiotropic)	+	+	+	?	1,3	GAS
	(IRF1>Lys6>IFP)						
	IL-11(Pleiotropic)	?	+	?	?	1,3	
	OnM(Pleiotropic)	?	+	+	?	1,3	
15	LIF(Pleiotropic)	?	+	+	?	1,3	
	CNTF(Pleiotropic)	-/+	+	+	?	1,3	
	G-CSF(Pleiotropic)	?	+	?	?	1,3	
	IL-12(Pleiotropic)	+	-	+	+	1,3	

g-C family

20	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP >>Ly6)(IgH)
	IL-7 (lymphocytes)	-	+	-	+	5	GAS
25	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS

gp140 family

30	IL-3 (myeloid)	-	-	+	-	5	GAS
	(IRF1>IFP>>Ly6)						
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS

Growth hormone family

GH	?	-	+	-	5	
PRL	?	+/-	+	-	1,3,5	
5 EPO	?	-	+	-	5	GAS(B-
CAS>IRF1=IFP>>Ly6)						

Receptor Tyrosine Kinases

EGF	?	+	+	-	1,3	GAS (IRF1)
10 PDGF	?	+	+	-	1,3	
CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 33-34, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., *Immunity* 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

10 5':GCGCCTCGAGATTCCCCGAAATCTAGATTCCCCGAAATGATTCCCC
GAAATGATTCCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:1549)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTGCAAAGCCTAGGC:3'
(SEQ ID NO:1550)

15 PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with Xhol/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

20 5':CTCGAGATTCCCCGAAATCTAGATTCCCCGAAATGATTCCCCGAAA
TGATTCCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTC
CCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTCCGCCATT
CCGCCCCCATGGCTGACTAATTTTTTTTATTTTATGCAGAGGCCGAGGCC
TCGGCCTCTGAGCTATTCCAGAACTAGTGAGGAGGGCTTTTTGGAGGCTA

25 GGCTTTGTCAAAAAGCT:3' (SEQ ID NO:1551)

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol

acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and 5 Xhol, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-
10 SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using Sall and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding
15 as described in Examples 33-34.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 35 and 36. However, many other promoters can be substituted using the protocols described
20 in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

25

Example 33: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors, and determining whether supernate containing a polypeptide of the invention
30 proliferates and/or differentiates T-cells. T-cell activity is assessed using the

GAS/SEAP/Neo construct produced in Example 32. Thus, factors that increase SEAP activity indicate the ability to activate the Jak-STATS signal transduction pathway.

The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC

5 Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies) (transfection procedure described below). The transfected cells are seeded to a density of approximately
10 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells
15 containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1% Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies) with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

20 During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final concentration of 10^7 cells/ml. Then add 1ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37 degree C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

25 The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Genticin, and 1% Pen-Strep. These cells are treated with supernatants containing polypeptide of the present invention or polypeptide of the present invention induced polypeptides as produced by the protocol described in Example 31.

30 On the day of treatment with the supernatant, the cells should be washed and

resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

- 5 Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100,000 cells per well).

After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12
10 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul
15 samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20 degree C until SEAP assays are performed according to Example 37. The plates containing the remaining treated cells are placed at 4 degree C and serve as a source of material for repeating the assay on a specific well if desired.

20 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

The above protocol may be used in the generation of both transient, as well as, stable transfected cells, which would be apparent to those of skill in the art.

25

Example 34: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity of polypeptide of the present invention by determining whether polypeptide of the present invention
30 proliferates and/or differentiates myeloid cells. Myeloid cell activity is assessed using

the GAS/SEAP/Neo construct produced in Example 32. Thus, factors that increase SEAP activity indicate the ability to activate the Jak-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

5 To transiently transfet U937 cells with the GAS/SEAP/Neo construct produced in Example 32, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml
10 penicillin and 100 mg/ml streptomycin.

Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM Na₂HPO₄.7H₂O, 1 mM MgCl₂, and 675 uM CaCl₂. Incubate at 37 degrees C for 45 min.

15 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37 degree C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

20 These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 ul cells per well in the 96-well plate (or 1×10^5 cells/well).

Add 50 ul of the supernatant prepared by the protocol described in Example
25 31. Incubate at 37 degee C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 37.

30 *Example 35: High-Throughput Screening Assay Identifying Neuronal Activity.*

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1-promoter-linked-to-reporter-molecules, activation of cells can be assessed by polypeptide of the present invention.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells by polypeptide of the present invention can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

20 5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO: 1552)

 5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO: 1553)

Using the GAS:SEAP/Neo vector produced in Example 32, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes Xhol/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter

sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 31. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 31, 37 degree C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ml of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 37.

Example 36: High-Throughput Screening Assay for T-cell Activity

NF-KB (Nuclear Factor KB) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF-KB regulates the expression of genes involved in immune cell activation, control of apoptosis (NF-KB appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF-KB is retained in the cytoplasm with I-KB (Inhibitor KB). However, upon stimulation, I-KB is phosphorylated and degraded, causing NF-KB to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF-KB include IL-2, IL-6, GM-CSF, ICAM-1 and class I MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF-KB promoter element are used to screen the supernatants produced in Example 31. Activators or inhibitors of NF-KB would be useful in treating, preventing, and/or diagnosing diseases. For example, inhibitors of NF-KB could be used to treat those diseases related to the acute or chronic activation of NF-KB, such as rheumatoid arthritis.

To construct a vector containing the NF-KB promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF-KB binding site (GGGGACTTCCC) (SEQ ID NO:1554), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an Xhol site:

5':GCGGCCTCGAGGGACTTCCCGGGACTTCCGGGACTTCCGGAC
25 TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:1555)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTGCAAAGCCTAGGC:3' (SEQ ID NO:1550)

PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is

digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene) Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

5':CTCGAGGGACTTCCCGGGACTTCCGGGACTTCCGGACTTTCC
5 ATCTGCCATCTCAATTAGTCAGCAACCATACTCCCCTAACTCCGCC
- - - - - ATCCCCTAACCTCCGCCAGTCCGCCATTCTCCGCCCATGGCTGA
CTAATTTTTTATTTATGCAGAGGCCGAGGCCCTCGGCCTTGAGCTA
TTCCAGAAGTAGTGAGGAGGCTTTGGAGGCCTAGGCTTGCAAAAAA
GCTT:3' (SEQ ID NO:1556)

10 Next, replace the SV40 minimal promoter element present in the pSEAP2-promoter plasmid (Clontech) with this NF-KB/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

15 In order to generate stable mammalian cell lines, the NF-KB/SV40/SEAP cassette is removed from the above NF-KB/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF-KB/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

20 Once NF-KB/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 33. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 33. As a positive control, exogenous TNF alpha (0.1,1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

25 *Example 37: Assay for SEAP Activity*

As a reporter molecule for the assays described in Examples 33-36, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, 30 Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 ul of 2.5x dilution buffer into Optiplates containing 35 ul of a supernatant. Seal the plates with a plastic sealer and incubate at 65 degree C for 30 min. Separate the Optiplates to avoid uneven heating.

5 Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 ml Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 ul Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it
10 takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

15 Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6
23	125	6.25
24	130	6.5

25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 38: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

5 Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol

describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to
5 measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-4 (Molecular Probes, Inc.; catalog no. F-14202), used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star
10 black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-4 is made in 10% pluronic acid DMSO. To load the cells with fluo-4, 50 ul of 12 μ g/ml fluo-4 is added to each well. The plate
15 is incubated at 37 degrees C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to $2\text{-}5 \times 10^6$ cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-4 solution in 10% pluronic acid DMSO is added to each ml of cell suspension.
20 The tube is then placed in a 37 degrees C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1×10^6 cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley Cell Wash with 200 ul, followed by an aspiration step to 100 ul final volume.
25 For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-4. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4
30 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm;

and (6) Sample addition is 50 μ l. Increased emission at 530 nm indicates an extracellular signaling event caused by the a molecule, either polypeptide of the present invention or a molecule induced by polypeptide of the present invention, which has resulted in an increase in the intracellular Ca^{++} concentration.

5

Example 40: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

15 Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, 20 members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, identifying whether polypeptide of the present invention or a molecule induced by polypeptide of the present invention is capable of activating tyrosine 25 kinase signal transduction pathways is of interest. Therefore, the following protocol is designed to identify such molecules capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from 30 Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with

100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or 5 calf serum, rinsed with PBS and stored at 4 degree C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are used to cover the Loprodynne Silent Screen 10 Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodynne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 15 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 31, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM Na₄P₂O₇ and a cocktail of protease inhibitors (# 1836170) obtained from Boeheringer Mannheim (Indianapolis, IN) is added to each well and the plate is 20 shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after 25 detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4 degree C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

30 Generally, the tyrosine kinase activity of a supernatant is evaluated by

determining its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for 5 a range of tyrosine kinases and are available from Boehringer Mannheim.

The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂₊ (5mM ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 10 0.5 mg/ml BSA); then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the components gently and preincubate the reaction mix at 30 degree C for 2 min. Initial the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mm EDTA and place the reactions on ice.

15 Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction mixture to a microtiter plate (MTP) module and incubating at 37 degree C for 20 min. This allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phospotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr- 20 POD(0.5u/ml)) to each well and incubate at 37 degree C for one hour. Wash the well as above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound 25 peroxidase activity is quantitated using an ELISA reader and reflects the level of tyrosine kinase activity.

Example 41: High-Throughput Screening Assay Identifying Phosphorylation Activity

30 As a potential alternative and/or compliment to the assay of protein tyrosine

kinase activity described in Example 40, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase, Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4 degree C until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyn filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 31 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation by polypeptide of the

present invention or a molecule induced by polypeptide of the present invention.

Example 42: Assay for the Stimulation of Bone Marrow CD34+ Cell Proliferation

5 This assay is based on the ability of human CD34+ to proliferate in the presence of hematopoietic growth factors and evaluates the ability of isolated polypeptides expressed in mammalian cells to stimulate proliferation of CD34+ cells.

It has been previously shown that most mature precursors will respond to only a single signal. More immature precursors require at least two signals to respond.

10 Therefore, to test the effect of polypeptides on hematopoietic activity of a wide range of progenitor cells, the assay contains a given polypeptide in the presence or absence of other hematopoietic growth factors. Isolated cells are cultured for 5 days in the presence of Stem Cell Factor (SCF) in combination with tested sample. SCF alone has a very limited effect on the proliferation of bone marrow (BM) cells, acting in
15 such conditions only as a "survival" factor. However, combined with any factor exhibiting stimulatory effect on these cells (e.g., IL-3), SCF will cause a synergistic effect. Therefore, if the tested polypeptide has a stimulatory effect on a hematopoietic progenitors, such activity can be easily detected. Since normal BM cells have a low level of cycling cells, it is likely that any inhibitory effect of a given polypeptide, or
20 agonists or antagonists thereof, might not be detected. Accordingly, assays for an inhibitory effect on progenitors is preferably tested in cells that are first subjected to *in vitro* stimulation with SCF+IL+3, and then contacted with the compound that is being evaluated for inhibition of such induced proliferation.

Briefly, CD34+ cells are isolated using methods known in the art. The cells
25 are thawed and resuspended in medium (QBSF 60 serum-free medium with 1% L-glutamine (500ml) Quality Biological, Inc., Gaithersburg, MD Cat# 160-204-101). After several gentle centrifugation steps at 200 x g, cells are allowed to rest for one hour. The cell count is adjusted to 2.5×10^5 cells/ml. During this time, 100 µl of sterile water is added to the peripheral wells of a 96-well plate. The cytokines that
30 can be tested with a given polypeptide in this assay is rhSCF (R&D Systems,

Minneapolis, MN, Cat# 255-SC) at 50 ng/ml alone and in combination with rhSCF and rhIL-3 (R&D Systems, Minneapolis, MN, Cat# 203-ML) at 30 ng/ml. After one hour, 10 µl of prepared cytokines, 50 µl of the supernatants prepared in Example 31 (supernatants at 1:2 dilution = 50 µl) and 20 µl of diluted cells are added to the media 5 which is already present in the wells to allow for a final total volume of 100 µl. The plates are then placed in a 37°C/5% CO₂ incubator for five days.

Eighteen hours before the assay is harvested, 0.5 µCi/well of [3H] Thymidine 10 is added in a 10 µl volume to each well to determine the proliferation rate. The experiment is terminated by harvesting the cells from each 96-well plate to a filtermat using the Tomtec Harvester 96. After harvesting, the filtermats are dried, trimmed 15 and placed into OmniFilter assemblies consisting of one OmniFilter plate and one OmniFilter Tray. 60 µl Microscint is added to each well and the plate sealed with TopSeal-A press-on sealing film. A bar code 15 sticker is affixed to the first plate for counting. The sealed plates are then loaded and the level of radioactivity determined via the Packard Top Count and the printed data collected for analysis. The level of 20 radioactivity reflects the amount of cell proliferation.

The studies described in this example test the activity of a given polypeptide 25 to stimulate bone marrow CD34+ cell proliferation. One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or antagonists and fragments and variants thereof. As a nonlimiting example, potential antagonists tested in this assay would be expected 30 to inhibit cell proliferation in the presence of cytokines and/or to increase the inhibition of cell proliferation in the presence of cytokines and a given polypeptide. In contrast, potential agonists tested in this assay would be expected to enhance cell proliferation and/or to decrease the inhibition of cell proliferation in the presence of cytokines and a given polypeptide.

The ability of a gene to stimulate the proliferation of bone marrow CD34+ 35 cells indicates that polynucleotides and polypeptides corresponding to the gene are useful for the diagnosis and treatment of disorders affecting the immune system and hematopoiesis. Representative uses are described in the "Immune Activity" and

"Infectious Disease" sections above, and elsewhere herein.

Example 43: Assay for Extracellular Matrix Enhanced Cell Response (EMECR)

5 The objective of the Extracellular Matrix Enhanced Cell Response (EMECR) assay is to identify gene products (e.g., isolated polypeptides) that act on the hematopoietic stem cells in the context of the extracellular matrix (ECM) induced signal.

Cells respond to the regulatory factors in the context of signal(s) received from
10 the surrounding microenvironment. For example, fibroblasts, and endothelial and epithelial stem cells fail to replicate in the absence of signals from the ECM. Hematopoietic stem cells can undergo self-renewal in the bone marrow, but not in *in vitro* suspension culture. The ability of stem cells to undergo self-renewal *in vitro* is dependent upon their interaction with the stromal cells and the ECM protein
15 fibronectin (fn). Adhesion of cells to fn is mediated by the $\alpha_5\beta_1$ and $\alpha_4\beta_1$ integrin receptors, which are expressed by human and mouse hematopoietic stem cells. The factor(s) which integrate with the ECM environment and responsible for stimulating stem cell self-renewal has not yet been identified. Discovery of such factors should be of great interest in gene therapy and bone marrow transplant applications

20 Briefly, polystyrene, non tissue culture treated, 96-well plates are coated with fn fragment at a coating concentration of 0.2 $\mu\text{g}/\text{cm}^2$. Mouse bone marrow cells are plated (1,000 cells/well) in 0.2 ml of serum-free medium. Cells cultured in the presence of IL-3 (5 ng/ml) + SCF (50 ng/ml) would serve as the positive control, conditions under which little self-renewal but pronounced differentiation of the stem
25 cells is to be expected. Gene products of the invention (e.g., including, but not limited to, polynucleotides and polypeptides of the present invention, and supernatants produced in Example 31), are tested with appropriate negative controls in the presence and absence of SCF(5.0 ng/ml), where test factor supernates represent 10% of the total assay volume. The plated cells are then allowed to grow by incubating in
30 a low oxygen environment (5% CO₂, 7% O₂, and 88% N₂) tissue culture incubator

for 7 days. The number of proliferating cells within the wells is then quantitated by measuring thymidine incorporation into cellular DNA. Verification of the positive hits in the assay will require phenotypic characterization of the cells, which can be accomplished by scaling up of the culture system and using appropriate antibody reagents against cell surface antigens and FACScan.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or antagonists and fragments and variants thereof.

If a particular polypeptide of the present invention is found to be a stimulator of hematopoietic progenitors, polynucleotides and polypeptides corresponding to the gene encoding said polypeptide may be useful for the diagnosis and treatment of disorders affecting the immune system and hematopoiesis. Representative uses are described in the "Immune Activity" and "Infectious Disease" sections above, and elsewhere herein. The gene product may also be useful in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types.

Additionally, the polynucleotides and/or polypeptides of the gene of interest and/or agonists and/or antagonists thereof, may also be employed to inhibit the proliferation and differentiation of hematopoietic cells and therefore may be employed to protect bone marrow stem cells from chemotherapeutic agents during chemotherapy. This antiproliferative effect may allow administration of higher doses of chemotherapeutic agents and, therefore, more effective chemotherapeutic treatment.

Moreover, polynucleotides and polypeptides corresponding to the gene of interest may also be useful for the treatment and diagnosis of hematopoietic related disorders such as, for example, anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia.

Example 44: Human Dermal Fibroblast and Aortic Smooth Muscle Cell Proliferation

The polypeptide of interest is added to cultures of normal human dermal fibroblasts (NHDF) and human aortic smooth muscle cells (AoSMC) and two co-assays are performed with each sample. The first assay examines the effect of the polypeptide of interest on the proliferation of normal human dermal fibroblasts (NHDF) or aortic smooth muscle cells (AoSMC). Aberrant growth of fibroblasts or smooth muscle cells is a part of several pathological processes, including fibrosis, and restenosis. The second assay examines IL6 production by both NHDF and SMC. IL6 production is an indication of functional activation. Activated cells will have increased production of a number of cytokines and other factors, which can result in a proinflammatory or immunomodulatory outcome. Assays are run with and without co-TNF α stimulation, in order to check for costimulatory or inhibitory activity.

Briefly, on day 1, 96-well black plates are set up with 1000 cells/well (NHDF) or 2000 cells/well (AoSMC) in 100 μ l culture media. NHDF culture media contains: Clonetics FB basal media, 1mg/ml hFGF, 5mg/ml insulin, 50mg/ml gentamycin, 2%FBS, while AoSMC culture media contains Clonetics SM basal media, 0.5 μ g/ml hEGF, 5mg/ml insulin, 1 μ g/ml hFGF, 50mg/ml gentamycin, 50 μ g/ml Amphotericin B, 5%FBS. After incubation at 37°C for at least 4-5 hours, culture media is aspirated and replaced with growth arrest media. Growth arrest media for NHDF contains fibroblast basal media, 50mg/ml gentamycin, 2% FBS, while growth arrest media for AoSMC contains SM basal media, 50mg/ml gentamycin, 50 μ g/ml Amphotericin B, 0.4% FBS. Incubate at 37°C until day 2.

On day 2, serial dilutions and templates of the polypeptide of interest are designed such that they always include media controls and known-protein controls. For both stimulation and inhibition experiments, proteins are diluted in growth arrest media. For inhibition experiments, TNF α is added to a final concentration of 2ng/ml (NHDF) or 5ng/ml (AoSMC). Add 1/3 vol media containing controls or polypeptides of the present invention and incubate at 37°C/5% CO $_2$ until day 5.

Transfer 60 μ l from each well to another labeled 96-well plate, cover with a plate-sealer, and store at 4°C until Day 6 (for IL6 ELISA). To the remaining 100 μ l in the cell culture plate, aseptically add Alamar Blue in an amount equal to 10% of the culture volume (10 μ l). Return plates to incubator for 3 to 4 hours. Then measure 5 fluorescence with excitation at 530nm and emission at 590nm using the CytoFluor. This yields the growth stimulation/inhibition data.

On day 5, the IL6 ELISA is performed by coating a 96 well plate with 50-100 μ l/well of Anti-Human IL6 Monoclonal antibody diluted in PBS, pH 7.4, incubate ON at room temperature.

10 On day 6, empty the plates into the sink and blot on paper towels. Prepare Assay Buffer containing PBS with 4% BSA. Block the plates with 200 μ l/well of Pierce Super Block blocking buffer in PBS for 1-2 hr and then wash plates with wash buffer (PBS, 0.05% Tween-20). Blot plates on paper towels. Then add 50 μ l/well of diluted Anti-Human IL-6 Monoclonal, Biotin-labeled antibody at 0.50 mg/ml. Make 15 dilutions of IL-6 stock in media (30, 10, 3, 1, 0.3, 0 ng/ml). Add duplicate samples to top row of plate. Cover the plates and incubate for 2 hours at RT on shaker. Plates are washed with wash buffer and blotted on paper towels. Dilute EU-labeled Streptavidin 1:1000 in Assay buffer, and add 100 μ l/well. Cover the plate and incubate 1 h at RT. Plates are again washed with wash buffer and blotted on paper towels. Add 100 20 μ l/well of Enhancement Solution and shake for 5 minutes. Read the plate on the Wallac DELFIA Fluorometer. Readings from triplicate samples in each assay are tabulated and averaged.

A positive result in this assay suggests AoSMC cell proliferation and that the polypeptide of the present invention may be involved in dermal fibroblast 25 proliferation and/or smooth muscle cell proliferation. A positive result also suggests many potential uses of polypeptides, polynucleotides, agonists and/or antagonists of the polynucleotide/polypeptide of the present invention which gives a positive result. For example, inflammation and immune responses, wound healing, and angiogenesis, as detailed throughout this specification. Particularly, polypeptides of the present 30 invention and polynucleotides of the present invention may be used in wound healing

and dermal regeneration, as well as the promotion of vasculargenesis, both of the blood vessels and lymphatics. The growth of vessels can be used in the treatment of, for example, cardiovascular diseases. Additionally, antagonists of polypeptides and polynucleotides of the invention may be useful in treating diseases, disorders, and/or conditions which involve angiogenesis by acting as an anti-vascular (e.g., anti-angiogenesis). These diseases, disorders, and/or conditions are known in the art and/or are described herein, such as, for example, malignancies, solid tumors, benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas; arteriosclerotic plaques; ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrobulbar fibroplasia, rubeosis, retinoblastoma, uveitis and Pterygia (abnormal blood vessel growth) of the eye; rheumatoid arthritis; psoriasis; delayed wound healing; endometriosis; vasculogenesis; granulations; hypertrophic scars (keloids); nonunion fractures; scleroderma; trachoma; vascular adhesions; myocardial angiogenesis; coronary collaterals; cerebral collaterals; arteriovenous malformations; ischemic limb angiogenesis; Osler-Webber Syndrome; plaque neovascularization; telangiectasia; hemophiliac joints; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; and atherosclerosis. Moreover, antagonists of polypeptides and polynucleotides of the invention may be useful in treating anti-hyperproliferative diseases and/or anti-inflammatory known in the art and/or described herein.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or antagonists and fragments and variants thereof.

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Example 45: Cellular Adhesion Molecule (CAM) Expression on Endothelial Cells

The recruitment of lymphocytes to areas of inflammation and angiogenesis involves specific receptor-ligand interactions between cell surface adhesion molecules

(CAMs) on lymphocytes and the vascular endothelium. The adhesion process, in both normal and pathological settings, follows a multi-step cascade that involves intercellular adhesion molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), and endothelial leukocyte adhesion molecule-1 (E-selectin) expression on 5 endothelial cells (EC). The expression of these molecules and others on the vascular endothelium determines the efficiency with which leukocytes may adhere to the local vasculature and extravasate into the local tissue during the development of an inflammatory response. The local concentration of cytokines and growth factor participate in the modulation of the expression of these CAMs.

- 10 Briefly, endothelial cells (e.g., Human Umbilical Vein Endothelial cells (HUVECs)) are grown in a standard 96 well plate to confluence, growth medium is removed from the cells and replaced with 100 μ l of 199 Medium (10% fetal bovine serum (FBS)). Samples for testing and positive or negative controls are added to the plate in triplicate (in 10 μ l volumes). Plates are then incubated at 37°C for either 5 h
15 (selectin and integrin expression) or 24 h (integrin expression only). Plates are aspirated to remove medium and 100 μ l of 0.1% paraformaldehyde-PBS (with Ca⁺⁺ and Mg⁺⁺) is added to each well. Plates are held at 4°C for 30 min. Fixative is removed from the wells and wells are washed 1X with PBS(+Ca,Mg) + 0.5% BSA and drained. 10 μ l of diluted primary antibody is added to the test and control wells.
20 Anti-ICAM-1-Biotin, Anti-VCAM-1-Biotin and Anti-E-selectin-Biotin are used at a concentration of 10 μ g/ml (1:10 dilution of 0.1 mg/ml stock antibody). Cells are incubated at 37°C for 30 min. in a humidified environment. Wells are washed three times with PBS(+Ca,Mg) + 0.5% BSA. 20 μ l of diluted ExtrAvidin-Alkaline Phosphotase (1:5,000 dilution, referred to herein as the working dilution) are added to
25 each well and incubated at 37°C for 30 min. Wells are washed three times with PBS(+Ca,Mg)+0.5% BSA. Dissolve 1 tablet of p-Nitrophenol Phosphate pNPP per 5 ml of glycine buffer (pH 10.4). 100 μ l of pNPP substrate in glycine buffer is added to each test well. Standard wells in triplicate are prepared from the working dilution of the ExtrAvidin-Alkaline Phosphotase in glycine buffer: 1:5,000 (10^0) > $10^{-0.5}$ > 10^{-1} >
30 $10^{-1.5}$. 5 μ l of each dilution is added to triplicate wells and the resulting AP content in

each well is 5.50 ng, 1.74 ng, 0.55 ng, 0.18 ng. 100 µl of pNNP reagent is then added to each of the standard wells. The plate is incubated at 37°C for 4h. A volume of 50 µl of 3M NaOH is added to all wells. The plate is read on a plate reader at 405 nm using the background subtraction option on blank wells filled with glycine buffer only. Additionally, the template is set up to indicate the concentration of AP-conjugate in each standard well [5.50 ng; 1.74 ng; 0.55 ng; 0.18 ng]. Results are indicated as amount of bound AP-conjugate in each sample.

Example 46: Alamar Blue Endothelial Cells Proliferation Assay

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This assay may be used to quantitatively determine protein mediated inhibition of bFGF-induced proliferation of Bovine Lymphatic Endothelial Cells (LECs), Bovine Aortic Endothelial Cells (BAECs) or Human Microvascular Uterine Myometrial Cells (UTMECs). This assay incorporates a fluorometric growth indicator based on detection of metabolic activity. A standard Alamar Blue Proliferation Assay is prepared in EGM-2MV with 10 ng /ml of bFGF added as a source of endothelial cell stimulation. This assay may be used with a variety of endothelial cells with slight changes in growth medium and cell concentration. Dilutions of the protein batches to be tested are diluted as appropriate. Serum-free medium (GIBCO SFM) without bFGF is used as a non-stimulated control and Angiostatin or TSP-1 are included as a known inhibitory controls.

Briefly, LEC, BAECs or UTMECs are seeded in growth media at a density of 5000 to 2000 cells/well in a 96 well plate and placed at 37-C overnight. After the overnight incubation of the cells, the growth media is removed and replaced with GIBCO EC-SFM. The cells are treated with the appropriate dilutions of the protein of interest or control protein sample(s) (prepared in SFM) in triplicate wells with additional bFGF to a concentration of 10 ng/ ml. Once the cells have been treated with the samples, the plate(s) is/are placed back in the 37° C incubator for three days. After three days 10 ml of stock alamar blue (Biosource Cat# DAL1100) is added to each well and the plate(s) is/are placed back in the 37°C incubator for four hours. The

plate(s) are then read at 530nm excitation and 590nm emission using the CytoFluor fluorescence reader. Direct output is recorded in relative fluorescence units.

Alamar blue is an oxidation-reduction indicator that both fluoresces and changes color in response to chemical reduction of growth medium resulting from cell growth. As cells grow in culture, innate metabolic activity results in a chemical reduction of the immediate surrounding environment. Reduction related to growth causes the indicator to change from oxidized (non-fluorescent blue) form to reduced (fluorescent red) form. i.e. stimulated proliferation will produce a stronger signal and inhibited proliferation will produce a weaker signal and the total signal is proportional to the total number of cells as well as their metabolic activity. The background level of activity is observed with the starvation medium alone. This is compared to the output observed from the positive control samples (bFGF in growth medium) and protein dilutions.

15 *Example 47: Detection of Inhibition of a Mixed Lymphocyte Reaction*

This assay can be used to detect and evaluate inhibition of a Mixed Lymphocyte Reaction (MLR) by gene products (e.g., isolated polypeptides). Inhibition of a MLR may be due to a direct effect on cell proliferation and viability, modulation of costimulatory molecules on interacting cells, modulation of adhesiveness between lymphocytes and accessory cells, or modulation of cytokine production by accessory cells. Multiple cells may be targeted by these polypeptides since the peripheral blood mononuclear fraction used in this assay includes T, B and natural killer lymphocytes, as well as monocytes and dendritic cells.

25 Polypeptides of interest found to inhibit the MLR may find application in diseases associated with lymphocyte and monocyte activation or proliferation. These include, but are not limited to, diseases such as asthma, arthritis, diabetes, inflammatory skin conditions, psoriasis, eczema, systemic lupus erythematosus, multiple sclerosis, glomerulonephritis, inflammatory bowel disease, crohn's disease, ulcerative colitis, arteriosclerosis, cirrhosis, graft vs. host disease, host vs. graft

disease, hepatitis, leukemia and lymphoma.

Briefly, PBMCs from human donors are purified by density gradient centrifugation using Lymphocyte Separation Medium (LSM®, density 1.0770 g/ml, Organon Teknica Corporation, West Chester, PA). PBMCs from two donors are 5 adjusted to 2×10^6 cells/ml in RPMI-1640 (Life Technologies, Grand Island, NY) supplemented with 10% FCS and 2 mM glutamine. PBMCs from a third donor is adjusted to 2×10^5 cells/ml. Fifty microliters of PBMCs from each donor is added to wells of a 96-well round bottom microtiter plate. Dilutions of test materials (50 µl) is added in triplicate to microtiter wells. Test samples (of the protein of interest) are 10 added for final dilution of 1:4; rhuIL-2 (R&D Systems, Minneapolis, MN, catalog number 202-IL) is added to a final concentration of 1 µg/ml; anti-CD4 mAb (R&D Systems, clone 34930.11, catalog number MAB379) is added to a final concentration of 10 µg/ml. Cells are cultured for 7-8 days at 37°C in 5% CO₂, and 1 µC of [³H] thymidine is added to wells for the last 16 hrs of culture. Cells are harvested and 15 thymidine incorporation determined using a Packard TopCount. Data is expressed as the mean and standard deviation of triplicate determinations.

Samples of the protein of interest are screened in separate experiments and compared to the negative control treatment, anti-CD4 mAb, which inhibits proliferation of lymphocytes and the positive control treatment, IL-2 (either as 20 recombinant material or supernatant), which enhances proliferation of lymphocytes.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or antagonists and fragments and variants thereof.

It will be clear that the invention may be practiced otherwise than as 25 particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other 30 disclosures) in the Background of the Invention, Detailed Description, and Examples

is hereby incorporated herein by reference. Further, the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both incorporated herein by reference in their entireties. Moreover, the hard copy of and the corresponding computer readable form of the Sequence Listing of Serial No. 5 60/124,270 are also incorporated herein by reference in their entireties.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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B. IDENTIFICATION OF DEPOSIT <input checked="" type="checkbox"/> <i>Further deposits are identified on an additional sheet</i>			
Name of depositary institution American Type Culture Collection			
Address of depositary institution <i>(including postal code and country)</i> 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America			
Date of deposit	20 May 1997	Accession Number	209059
C. ADDITIONAL INDICATIONS <i>(leave blank if not applicable)</i>		This information is continued on an additional sheet <input checked="" type="checkbox"/>	
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Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).			
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AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

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ATCC Deposit No.: 209059

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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Name of depositary institution American Type Culture Collection			
Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America			
Date of deposit	20 May 1997	Accession Number	209060
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D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).			
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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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<p>B. IDENTIFICATION OF DEPOSIT <input checked="" type="checkbox"/> Further deposits are identified on an additional sheet</p> <p>Name of depositary institution American Type Culture Collection</p>			
<p>Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</p>			
Date of deposit	20 May 1997	Accession Number	209061
<p>C. ADDITIONAL INDICATIONS <i>(leave blank if not applicable)</i></p>		<p>This information is continued on an additional sheet <input checked="" type="checkbox"/></p>	
<p>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE <i>(if the indications are not for all designated States)</i></p> <p>Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).</p>			
<p>E. SEPARATE FURNISHING OF INDICATIONS <i>(leave blank if not applicable)</i></p> <p>The indications listed below will be submitted to the International Bureau later <i>(specify the general nature of the indications e.g. "Accession Number of Deposit")</i></p>			
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NORWAY

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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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ATCC Deposit No.: 209061

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<p>A. The indications made below relate to the microorganism referred to in the description on page <u>91</u>, line <u>N/A</u></p>			
<p>B. IDENTIFICATION OF DEPOSIT <input checked="" type="checkbox"/> Further deposits are identified on an additional sheet</p>			
<p>Name of depository institution American Type Culture Collection</p>			
<p>Address of depository institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</p>			
Date of deposit	20 May 1997	Accession Number	209062
<p>C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>)</p>		<p>This information is continued on an additional sheet <input type="checkbox"/></p>	
<p>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)</p> <p>Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).</p>			
<p>E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>)</p> <p>The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications e.g., "Accession Number of Deposit"</i>)</p>			
<p>For receiving Office use only</p> <p><input type="checkbox"/> This sheet was received with the international application</p>		<p>For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p>	
<p>Authorized officer</p>		<p>Authorized officer</p>	

ATCC Deposit No.: 209062

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

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ATCC Deposit No.: 209062

DENMARK

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NETHERLANDS

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

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<p>B. IDENTIFICATION OF DEPOSIT</p>		Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection			
Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America			
Date of deposit	Accession Number		
20 May 1997	209063		
<p>C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>)</p>		This information is continued on an additional sheet <input type="checkbox"/>	
(Leave blank if not applicable)			
<p>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)</p>			
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).			
<p>E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>)</p>			
The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications e.g., "Accession Number of Deposit"</i>)			
For receiving Office use only		For International Bureau use only	
<input type="checkbox"/> This sheet was received with the international application		<input type="checkbox"/> This sheet was received by the International Bureau on:	
Authorized officer		Authorized officer	

ATCC Deposit No.: 209063

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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ATCC Deposit No.: 209063

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>		
B. IDENTIFICATION OF DEPOSIT		Further deposits are identified on an additional sheet <input type="checkbox"/>
Name of depositary institution American Type Culture Collection		
Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America		
Date of deposit <u>20 May 1997</u>	Accession Number <u>209064</u>	
C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>)		This information is continued on an additional sheet <input type="checkbox"/>
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).		
E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>) The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications e.g. "Accession Number of Deposit"</i>)		
For receiving Office use only <input type="checkbox"/> This sheet was received with the international application		For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer		Authorized officer

ATCC Deposit No.: 209064

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

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ATCC Deposit No.: 209064

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u>, line <u>N/A</u>		
B. IDENTIFICATION OF DEPOSIT <input checked="" type="checkbox"/> <i>Further deposits are identified on an additional sheet</i>		
Name of depositary institution American Type Culture Collection		
Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America		
Date of deposit 20 May 1997	Accession Number 209065	
C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>) <input type="checkbox"/> This information is continued on an additional sheet		
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).		
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For receiving Office use only <input type="checkbox"/> This sheet was received with the international application		For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer		Authorized officer

ATCC Deposit No.: 209065**CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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ATCC Deposit No.: 209065

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<p>A. The indications made below relate to the microorganism referred to in the description on page <u>91</u>, line <u>N/A</u></p>			
<p>B. IDENTIFICATION OF DEPOSIT</p>		Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection			
<p>Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</p>			
Date of deposit	20 May 1997	Accession Number	209066
<p>C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>)</p>		This information is continued on an additional sheet <input type="checkbox"/>	
<p>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)</p> <p>Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).</p>			
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<p>For receiving Office use only</p> <p><input type="checkbox"/> This sheet was received with the international application</p>		<p>For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p>	
Authorized officer		Authorized officer	

ATCC Deposit No.: 209066

CANADA

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FINLAND

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<p>A. The indications made below relate to the microorganism referred to in the description on page <u>91</u>, line <u>N/A</u></p>			
<p>B. IDENTIFICATION OF DEPOSIT</p>		Further deposits are identified on an additional sheet <input type="checkbox"/>	
<p>Name of depository institution American Type Culture Collection</p>			
<p>Address of depository institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</p>			
Date of deposit	20 May 1997	Accession Number	209067
<p>C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>)</p>		This information is continued on an additional sheet <input type="checkbox"/>	
<p>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)</p>			
<p>Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).</p>			
<p>E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>)</p>			
<p>The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications e.g., "Accession Number of Deposit"</i>)</p>			
<p>For receiving Office use only</p>		<p>For International Bureau use only</p>	
<input type="checkbox"/> This sheet was received with the international application		<input type="checkbox"/> This sheet was received by the International Bureau on:	
<p>Authorized officer</p>		<p>Authorized officer</p>	

ATCC Deposit No.: 209067

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

ATCC Deposit No.: 209067

DENMARK

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SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<p>A. The indications made below relate to the microorganism referred to in the description on page <u>91</u>, line <u>N/A</u></p>		
<p>B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/></p> <p>Name of depositary institution American Type Culture Collection</p>		
<p>Address of depositary institution <i>(including postal code and country)</i> 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</p>		
Date of deposit	Accession Number	
20 May 1997	209068	
<p>C. ADDITIONAL INDICATIONS <i>(leave blank if not applicable)</i> This information is continued on an additional sheet <input type="checkbox"/></p>		
<p>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE <i>(if the indications are not for all designated States)</i></p> <p>Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).</p>		
<p>E. SEPARATE FURNISHING OF INDICATIONS <i>(leave blank if not applicable)</i></p> <p>The indications listed below will be submitted to the International Bureau later <i>(specify the general nature of the indications e.g. "Accession Number of Deposit")</i></p>		
<p>For receiving Office use only</p> <p><input type="checkbox"/> This sheet was received with the international application</p>		
<p>For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p>		
<p>Authorized officer</p>		
<p>Authorized officer</p>		

ATCC Deposit No.: 209068

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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ATCC Deposit No.: 209068

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA102PGT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<p>A. The indications made below relate to the microorganism referred to in the description on page <u>91</u>, line <u>N/A</u></p>			
B. IDENTIFICATION OF DEPOSIT		<small>Further deposits are identified on an additional sheet</small> <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection			
Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America			
Date of deposit <u>20 May 1997</u>	Accession Number <u>209069</u>		
C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>)		<small>This information is continued on an additional sheet</small> <input type="checkbox"/>	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).			
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)			
The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications e.g., "Accession Number of Deposit"</i>)			
E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>)			
For receiving Office use only <input type="checkbox"/> This sheet was received with the international application		For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on:	
Authorized officer		Authorized officer	

ATCC Deposit No.: 209069

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

ATCC Deposit No.: 209069

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>		
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>		
Name of depositary institution <u>American Type Culture Collection</u>		
Address of depositary institution (<i>including postal code and country</i>) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>		
Date of deposit <u>12 January 1998</u>	Accession Number	<u>209579</u>
C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>) This information is continued on an additional sheet <input type="checkbox"/>		
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)		
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).		
E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>)		
The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications e.g., "Accession Number of Deposit"</i>)		
For receiving Office use only		For International Bureau use only
<input type="checkbox"/> This sheet was received with the international application		<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer		Authorized officer

ATCC Deposit No.: 209579

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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ATCC Deposit No.: 209579

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA.102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>			
B. IDENTIFICATION OF DEPOSIT		Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection			
Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America			
Date of deposit	12 January 1998	Accession Number	209578
C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>)		This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>) Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).			
E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>) The indications listed below will be submitted to the International Bureau later <i>(specify the general nature of the indications e.g., "Accession Number of Deposit")</i>			
For receiving Office use only		For International Bureau use only	
<input type="checkbox"/> This sheet was received with the international application		<input type="checkbox"/> This sheet was received by the International Bureau on:	
Authorized officer		Authorized officer	

ATCC Deposit No.: 209578

CANADA

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NORWAY

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FINLAND

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UNITED KINGDOM

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ATCC Deposit No.: 209578

DENMARK

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>			
B. IDENTIFICATION OF DEPOSIT		Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>			
Address of depositary institution (<i>including postal code and country</i>) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>			
Date of deposit <u>16 July 1998</u>	Accession Number <u>203067</u>		
C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>)		This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)			
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ATCC Deposit No.: 203067

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

ATCC Deposit No.: 203067

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<p>A. The indications made below relate to the microorganism referred to in the description on page <u>91</u>, line <u>N/A</u></p>			
<p>B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/></p>			
<p>Name of depositary institution American Type Culture Collection</p>			
<p>Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</p>			
Date of deposit	16 July 1998	Accession Number	203068
<p>C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>) This information is continued on an additional sheet <input type="checkbox"/></p>			
<p>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)</p> <p>Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).</p>			
<p>E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>)</p> <p>The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications e.g., "Accession Number of Deposit"</i>)</p>			
<p>For receiving Office use only</p> <p><input type="checkbox"/> This sheet was received with the international application</p>		<p>For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p>	
<p>Authorized officer</p>		<p>Authorized officer</p>	

ATCC Deposit No.: 203068

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

ATCC Deposit No.: 203068

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> , line <u>N/A</u>		
B. IDENTIFICATION OF DEPOSIT <input type="checkbox"/> Further deposits are identified on an additional sheet		
Name of depositary institution <u>American Type Culture Collection</u>		
Address of depositary institution (<i>including postal code and country</i>) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>		
Date of deposit <u>01 February 1999</u>	Accession Number <u>203609</u>	
C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>) <input type="checkbox"/> This information is continued on an additional sheet		
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>) <u>Europe</u> In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).		
E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>) The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications e.g., "Accession Number of Deposit"</i>)		
For receiving Office use only		For International Bureau use only
<input type="checkbox"/> This sheet was received with the international application		<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer		Authorized officer

ATCC Deposit No.: 203609

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

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FINLAND

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UNITED KINGDOM

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ATCC Deposit No.: 203609

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<p>A. The indications made below relate to the microorganism referred to in the description on page <u>91</u>, line <u>N/A</u></p>			
<p>B. IDENTIFICATION OF DEPOSIT</p>		<input type="checkbox"/> Further deposits are identified on an additional sheet	
<p>Name of depositary institution <u>American Type Culture Collection</u></p>			
<p>Address of depositary institution (<i>including postal code and country</i>) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u></p>			
Date of deposit	01 February 1999	Accession Number	203610
<p>C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>)</p>		<input type="checkbox"/> This information is continued on an additional sheet	
<p>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)</p>			
<p>Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).</p>			
<p>E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>)</p>			
<p>The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications e.g., "Accession Number of Deposit"</i>)</p>			
<p>For receiving Office use only</p>		<p>For International Bureau use only</p>	
<input type="checkbox"/> This sheet was received with the international application		<input type="checkbox"/> This sheet was received by the International Bureau on:	
<p>Authorized officer</p>		<p>Authorized officer</p>	

45.

ATCC Deposit No.: 203610**CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

ATCC Deposit No.: 203610

DENMARK

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SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<p>A. The indications made below relate to the microorganism referred to in the description on page <u>91</u>, line <u>N/A</u></p>			
<p>B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/></p>			
<p>Name of depositary institution American Type Culture Collection</p>			
<p>Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</p>			
Date of deposit	17 November 1998	Accession Number	203485
<p>C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>) This information is continued on an additional sheet <input type="checkbox"/></p>			
<p>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)</p> <p>Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).</p>			
<p>E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>)</p> <p>The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications e.g. "Accession Number of Deposit"</i>)</p>			
<p>For receiving Office use only</p> <p><input type="checkbox"/> This sheet was received with the international application</p> <p>Authorized officer</p>		<p>For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p> <p>Authorized officer</p>	

ATCC Deposit No.: 203485

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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ATCC Deposit No.: 203485

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>91</u> line <u>N/A</u>		
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>		
Name of depositary institution American Type Culture Collection		
Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America		
Date of deposit	Accession Number	
18 June 1999	PTA-252	
C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>) This information is continued on an additional sheet <input type="checkbox"/>		
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)		
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).		
E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>)		
The indications listed below will be submitted to the International Bureau later <i>(specify the general nature of the indications e.g., "Accession Number of Deposit")</i>		
For receiving Office use only		For International Bureau use only
<input type="checkbox"/> This sheet was received with the international application		<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer		Authorized officer

ATCC Deposit No.: PTA-252**CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

ATCC Deposit No.: PTA-252

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

-Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<p>A. The indications made below relate to the microorganism referred to in the description on page <u>91</u>, line <u>N/A</u>.</p>			
<p>B. IDENTIFICATION OF DEPOSIT</p>		Further deposits are identified on an additional sheet <input type="checkbox"/>	
<p>Name of depositary institution American Type Culture Collection</p>			
<p>Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</p>			
Date of deposit	18 June 1999	Accession Number	PTA-253
<p>C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>)</p>		This information is continued on an additional sheet <input type="checkbox"/>	
<p>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)</p> <p>Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).</p>			
<p>E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>)</p> <p>The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications e.g., "Accession Number of Deposit"</i>)</p>			
<p>For receiving Office use only</p> <input type="checkbox"/> This sheet was received with the international application		<p>For International Bureau use only</p> <input type="checkbox"/> This sheet was received by the International Bureau on:	
Authorized officer		Authorized officer	

ATCC Deposit No.: PTA-253**CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

ATCC Deposit No.: PTA-253

DENMARK

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SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA102PCT	International application No.	UNASSIGNED
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<p>A. The indications made below relate to the microorganism referred to in the description on page <u>91</u>, line <u>N/A</u></p>			
<p>B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/></p>			
<p>Name of depositary institution American Type Culture Collection</p>			
<p>Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</p>			
Date of deposit	22 December 1999	Accession Number	PTA-1081
<p>C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>) This information is continued on an additional sheet <input type="checkbox"/></p>			
<p>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)</p> <p>Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).</p>			
<p>E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>)</p> <p>The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications e.g., "Accession Number of Deposit"</i>)</p>			
<p>For receiving Office use only</p> <p><input type="checkbox"/> This sheet was received with the international application</p>		<p>For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p>	
<p>Authorized officer</p>		<p>Authorized officer</p>	

ATCC Deposit No.: PTA-1081**CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material-referred-to-in-the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

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ATCC Deposit No.: PTA-1081

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NETHERLANDS

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What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:
 - (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
 - (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
 - (c) a polynucleotide encoding a polypeptide fragment of a polypeptide encoded by SEQ ID NO:X or a polypeptide fragment encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
 - (d) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
 - (e) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;
 - (f) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X, having biological activity;
 - (g) a polynucleotide which is a variant of SEQ ID NO:X;
 - (h) a polynucleotide which is an allelic variant of SEQ ID NO:X;
 - (i) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;
 - (j) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide

sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a protein.

5

3. -- The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X.

10

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X.

15

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

20

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

25

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

30

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.
 11. An isolated polypeptide comprising an amino acid sequence at least 5 95% identical to a sequence selected from the group consisting of:
 - (a) a polypeptide fragment of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;
 - (b) a polypeptide fragment of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone, having biological activity;
 - 10 (c) a polypeptide domain of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;
 - (d) a polypeptide epitope of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;
 - (e) a full length protein of SEQ ID NO:Y or of the sequence encoded by the 15 cDNA included in the related cDNA clone;
 - (f) a variant of SEQ ID NO:Y;
 - (g) an allelic variant of SEQ ID NO:Y; or
 - (h) a species homologue of the SEQ ID NO:Y.
- 20 12. The isolated polypeptide of claim 11, wherein the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.
 13. An isolated antibody that binds specifically to the isolated polypeptide 25 of claim 11.
 14. A recombinant host cell that expresses the isolated polypeptide of claim 11.
 - 30 15. A method of making an isolated polypeptide comprising:

- (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
(b) recovering said polypeptide.

5 16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

10

18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and

15 (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

20 (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

25 20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

(a) contacting the polypeptide of claim 11 with a binding partner; and
(b) determining whether the binding partner effects an activity of the polypeptide.

30

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

22. A method of identifying an activity in a biological assay, wherein the
method comprises:

- 5 (a) expressing SEQ ID NO:X in a cell;
 (b) isolating the supernatant;
 (c) detecting an activity in a biological assay; and
 (d) identifying the protein in the supernatant having the activity.

10 23. The product produced by the method of claim 20.

SEQUENCE LISTING

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Steve Ruben

<120> Human Colon Cancer Associated Gene Sequences and Polypeptides

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cccataatgg tcttcactt gtcattctac ttcttatatt gttatcagtc cagggaaacag 480
gtaaacagat gtaatttagag acattggctc tttgttttagg cctaattttt ctttttactt 540
tttttttctt ttttctttt ttttaaagat catgaattt tgacttagtt ctgccccytg 600
gagaacaaaa gaaaggcagtc ttccatcaa tcaccttaaa atgcacggct aaactattca 660
gagttAACAC tccagaattt ttaaattaca agtactatgc tttaatgctt ctttcatctt 720
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agaagataga atccagggtt angg 804

<210> 8
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (714)
<223> n equals a,t,g, or c

<400> 8
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ccctgcagag gtccagggga cccaacagcc ccagcaagat gagatgccta gcccggacctt 180
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gctgaagggg gaggagtaac agccagaccc cccatcgtg gacaagggga gagtccccta 420
ctccccctgtat cccccaggtt cagactgagc tcccccttcc cagtagctct tgcatctcc 480
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tggcactgct ttcttgagga ctcaagggtgc caagatggag gggctgactc agtccagcc 600
acatttatgt agcacctact ttatgtatgg agctctaacc catgggtcca tggaaataaa 660
gcagtgaata gtaacaataa ataattgtaa cagaaaaaaaaaaaaaaa 720

<210> 9
<211> 540
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (463)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (524)
<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (535)

<223> n equals a,t,g, or c

<400> 9

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ctgtgttctc acatggcaga aggggcaaaac aagccccctt gggccttttataaaggca 180
cttaactctat gcctaaaggc agggccctca tgactctatc acctacaaa aggctccact 240
tctttatact attggagggg tagaaggaac ttcccttcta gaccttgaag gtttaagaat 300
ttgaatctat aaaacaagct gacaatagac agattaacag gagaaaaagc atatacattt 360
ttaatgtgg gccagatggc agaagcttaa ataacacccc aagctacagg gaagtgaggc 420
ctctgatggg ggaggttagt gacacaggct gtggggaggg gtnaggggga ggaatctgt 480
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<210> 10

<211> 561

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (406)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (450)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (546)

<223> n equals a,t,g, or c

<400> 10

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tgatgccatc ttatcatggc cagaccgaga gaagggcaaa ctccctngcat ggtcagaatg 420
gtctgttacc caacgggcag acccctctgn aaggccagga gcccgggaa rgagatccctg 480
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aacttnccga gttttcgggg g 561

<210> 11

<211> 393

<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (346)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (381)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (383)
<223> n equals a,t,g, or c

<400> 11
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tagaaccacg caagattcac ctgtgttttg tggtcatgtt cattgcctc taaaaggcaa 180
gggttgaaga taaaataaggt agcaatgtct atagtttgg ccttaactat gccaatctaa 240
ttataattcc ctgtatttaa aatggttct ttacttattt gaaaggcatt ttagtgtgg 300
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ccccctgggg gtcccaagct nancgtacgc ggg 393

<210> 12
<211> 322
<212> DNA
<213> Homo sapiens

<400> 12
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ccattgcact ccagccctggg ggacaagagt gaatctgtt ctcacccaaaa aaaaaaaaaagaa 180
aaagaaaagat gcttaacaaa ggttaccata agccacaaat tcatraccac ttatccttcc 240
agtttcaagt agaatatatt cataacctca ataaagttct ccctgctccc aaaaaaaaaaa 300
aaaaaaaaaaaa aaaaaaaaaaa ag 322

<210> 13
<211> 1907
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1834)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1843)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1888)

<223> n equals a,t,g, or c

<400> 13

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catcattaag gtttagtctg cccagatcac ctattagta ctaatttata tattctgaat 180
taaaattatc tgtaattta aaaacatttt atctattgtc ttcaaaaata gtattaactg 240
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gttttagaag gaaaaaacctt tcagctctac tctcacaatc ttatagctt gtttgaacat 360
gc当地aaaaac caggattagc tgcccatatt caaactcaca gggttccaga cc当地atacta 420
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atagtcgaa acccttacac gggacataaa tacctctgt gagcttaca gcttggaaatt 540
gttttacttc agtggtatga gc当地atgcag aaattcatgt tgataaaagca ctttgatttt 600
ccttgc当地aa gtccttggaa tggttttggaa atgctggta tacctgaaca ggaataaccct 660
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atcaatttga actctgc当地t ttcatggttt acagaaattt gtcaggcag cc当地caggtt 780
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aaacatggga tgcagggtaa aagcttcaag tc当地atgagg ttaccaggaa gatccagat 1020
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tttgagggtt tgggggtcaa cacacacatg caatttgc当地 aacaaaagta tttataata 1800
cagttcatac agaataaccyt aaaaggagc ytangttcc acnacagata agtggtaagg 1860
gtcataccgg agataatgtt gatagtgnaa tatccttagaa ggggggtt 1907

<210> 14

<211> 1140

<212> DNA

<213> Homo sapiens

<400> 14

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agtgc当地tga tgctttgc当地 aaaaacagaa taattcactg tgaccttaag cccgagaaca 120
ttttgttaaa gc当地cagggtt agaaggcgta taaaagtaat tgatcttgc tccagttgtt 180
acgagcatca gc当地gtctac acgttacatcc agtgc当地tgc ttaccgggtt cc当地aagtga 240

tccttggggc caggatggc atgcccattg atatgtggag cctgggctgc atttttagca 300
agctcctgac gggtaaaaaa ctcttgcctg gggaaagatga aggggaccag ctggcctgta 360
tgattgaact gttgggcatg cctcacagaa actgctggat gcacccaaac gagccaaaaa 420
ttttgtgagc tccaagggtt atccccgtta ctgcaactgtc acgactctct cagatggctc 480
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gagtggggka acgcgctgaa ggggtgtgat gatccccttt tcctgactt cttaaaacag 600
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<210> 15

<211> 2008

<212> DNA

<213> Homo sapiens

<400> 15

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gacacttagg gacaggtcac taagcagaat aggtattagt tggttttta ttatTTTaa 180
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gggcttggaaa actgcccag attaaagagc taagatgaaa tagttgaat aaactgttaa 360
aataacaatt catactatct ctacatattt ttaggatatg aaaaaaaaaa tcctgctggg 420
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gctattatat gctgtggctt tgagaagttt acctttgtgg aatatgaaac caaaggaaga 600
atttccatgt agataaaatta agaataggga aaaacatcta cctaaaagat gttgtccct 660
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aatggaaaaat ttatatgtat ttttaccaca ataaaacaaaa aaccctaaaa aaactttaat 1920
gaaagggtgga aaataattt acttayaatg tgaaaataca atgtgaaatg tacaataaat 1980
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<210> 16

<211> 371

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (350)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (360)

<223> n equals a,t,g, or c

<400> 16

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ataaaatcttg aggctgaggg cgggtggtac agatgtgtat gggaaacccc aaccctata 180
tattgtaaat agatgggctg ggctaaacat tggccgtt tcatacttct accaactcag 240
cttttacaca ataaagctct actgtctctg aaaaaaaaaaaaaaaa 300
aaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaattn ggggggggggn 360
cccccccccc c 371

<210> 17

<211> 763

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (6)

<223> n equals a,t,g, or c

<400> 17

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ggaAGCactt ctgtgtCAA gcaggcAGCC catggggTT catcttcCTG ttgggggATC 180
atccatTTTC ttcaatGAAT agtttAAgt ctgtcaaAT gtcacacAG agggccgcta 240
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cattcgggCA tggcatta gggatgACAT tctctGAAGG ctgcccggCT tgaatggCCA 360
aatccCTGCA tcatggCTT CTTAATTCC ctctgCTCCC aactcacAAA atgaggACCT 420
ctcttttaAG acgarAAAGG cactgttCCt caaaggTATA catttggAAC ttcaataatG 480
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ctctggatga tacggtatca aacactgctg ctccttctg tttcttttggaaagg 660
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<210> 18
<211> 1926
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (898)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1024)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1083)
<223> n equals a,t,g, or c

<400> 18
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magaaa 1926

<210> 19

<211> 2301

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (190)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2052)

<223> n equals a,t,g, or c

<400> 19

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ccttacgcattt ggtattcatg atgggtccct atctaagttc aggactgttt tcctacagcg 360
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<210> 20
<211> 538
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (507)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (514)
<223> n equals a,t,g, or c

<400> 20
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catctccgccc ctgagtctca tcactctgtc caccgtgttc aacctggccca gccccctcaa 180
cgccatgcag atcctatggta tcaacatcat catggatggg ccaccggggca gaggtgaggc 240
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<210> 21
<211> 1403
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1370)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (1386)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1393)

<223> n equals a,t,g, or c

<400> 21

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<210> 22

<211> 478

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (474)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (475)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (476)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (478)

<223> n equals a,t,g, or c

-> <400> 22

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tggaggcgct tgtaataaca aattgcttagg ccacaacctt aaagttctg attcagggtta 120
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ggccgggcgc ggtggctcac gcctgtatc ccagcactt gggaggccga ggtggggcgg 240
tcacaagtc aggagatcga gaccatcctg gctaacacgg tgaaccctg tctgttagtaa 300
aaataaaaaa aaattagcca ggcattgtgg tgggtgcctg tagtcccagc tacttggag 360
gctgaggcgag gagaatggtg tgaaccagg aggtggagct tgcagtgagc cgagatcg 420
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<210> 23

<211> 1252

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1227)

<223> n equals a,t,g, or c

<400> 23

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tgccttgggc tcctggcgca gcagatcatc ttcttcctgg gaaccacggc cttggccttc 180
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tgggtcttcc tggagactca tggatggacac ccacagctga ccaaccggcg agtgctctat 360
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<210> 24
<211> 1074
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (928)-
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (934)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1028)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1031)
<223> n equals a,t,g, or c

<400> 24
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cgccctggga cctgcactg tggcgtcgcc ctccctcccg cgccgcgagg ccgcgcaccc 720
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gcatgcgaag tcataactct ctccctataa tgatcgtatt ataagtaagc actggccgtc 1020
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<210> 25
<211> 1186
<212> DNA
<213> Homo sapiens

<400> 25

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gaccggcaga ccagccttct ggaacagggc cacattgtcc attacctgtc acaggtcctc 180
atcccgagcc ccaaggacca aacagtattc caacacccat tgcttcaggg ttctgtcctc 240
atcttggcgc tggcccttg ccacatgggg ttcaaggacc tcagcaggca tctccagtgc 300
ctggacagat tccaattcac agagcacagg tgccaccaac atttcaaaac aattaccatg 360
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<210> 26
<211> 888
<212> DNA
<213> *Homo sapiens*

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<220>
<221> misc feature
<222> (670)
<223> n equals a,t,q, or c
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<220>
<221> misc feature
<222> (675)
<223> n equals a,t,q, or c
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<400> 26
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caaggggctg accacagtgt tttcaggcat cgggcagccg gccttccagg tagggggcc 780
cagcaggagc ctgcgacccq gttccctqq ccctaqqcga ccqqqcgctc agccccaccq 840

cttctccctg cagcccgatt cgccgctgcc ttctgtgtca cctgcact 888

<210> 27

<211> 789

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (420)

<223> n equals a,t,g, or c

<400> 27

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tacgatgagc tacacaaggc tcattactta tttggtggaa atccaggaaa atcttgctct 180
ccaaagatga gattagatga ctctggtca ctgaagttgt gttagaccttc aaaagattat 240
ttactgaggc attgcaagta cctcataaga aaacacakgt ttgaagaaaa ggcccaagt 300
gatcccccta gtgctctgaa atatttacaa aatgatctt atataactgt ggatcattca 360
gaccsagaag agacaaaaga gttcagctc ctggcatcag ctctattcaa atctggttcn 420
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ctttgacacc ttagtaaatt tctttcctga cagcatgact cctcctaaag gcaacctggt 540
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tttccgtcy tttggattgc agtccactg actgacagta aagctgcagt gattgaggac 660
tgcaccagag ttctgaaggg atcttaacca tcacaagttt ttaccctt ctttcattgcc 720
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atactttcc 789

<210> 28

<211> 847

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (799)

<223> n equals a,t,g, or c

<400> 28

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acccctgtcg tattcttatta gaggtcaagc catcaactgaa gccatattca aggagaggga 180
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gcccccaatgt ggaacacagt tccagctgg ggtggcattc cttatcacca gctcttcaga 720

atccctcaatc ctaacaaggc cccctgcgg ctaaagctgc gctcaactacg accacttca 780
ccagtcggtg caggagatnt ttgaggtgaa caactgcctg tggaatcgtg gcagtaatgt 840
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<210> 29

<211> 666

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (4)

<223> n equals a,t,g, or c

<400> 29

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tacacatatg tatataataca tagtctatattt attctatata agaataatattt ccaataagaa 600
tatattccat acggaaatattt attagtcattt gatgtattt gccggtaaaa tt当地agata 660
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<210> 30

<211> 517

<212> DNA

<213> Homo sapiens

<400> 30

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c当地ccgctcg c当地gtccccc gtc当地tctc gtc当地ccggcc gccatcatgc tggc当地ctcat 180
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cagtaagat atgataccca cagtgccctt caacatgagg aaggtaacta aaggtaacgt 360
cacaataaag atctggaca taggaggaca acccc当地t cgaagcatgt gggagc当地ta 420
ttgc当地agaga gtcaatgcta tt当地ttacat gataagatgtt gcaagatcgtg aaaagataga 480
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<210> 31

<211> 2675

<212> DNA

<213> Homo sapiens

<400> 31

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gcagaaaatga aaactgaaga tggcaaagta gaaaaaacact atctcttcta tgacggagaa 240
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<210> 32
<211> 277
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (109)
<223> n equals a,t,g, or c

<400> 32

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ccagggtcg agacctcgga gtctctcagt gactcactct acgactcgnt gtcctcttgt 120
gggagtcaagg gctgaggggc tgccacgc cacggccccc ctggagctgg ggaccacaga 180
ctggaccggc tctcttcatg cccagccccc ggagacgggg accccctccc-tgaagggacc 240
aaggaggcag gtggataaga aggttggaaaa gggggtt 277

<210> 33

<211> 921
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (2)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (839)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (846)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (886)
<223> n equals a,t,g, or c

<400> 33

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ttcatccacc tctgtggacg atgcattcc tttaccactt cctgtccac aacctaaagca 180
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tgtacccccc catcacaata aattggagca gcaccaagt tatggtgcca ggtcagagcc 360
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acaccactcc aagccatgca gccgggtcga gtagtgcatttcttgcact cctctgtcag 480
gaatacctgt taccggaaat acatccacc gtaccctacc atccggagag tgcagtctct 540
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agatgtgatg ccagcctact gccaagacc tctgtaccaa tataagccat atcagtcctc 660
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ccactacagg tataccccat attccatc ttcttagttcc tattacagtc cagatggggc 780
cctgtgtat gtggatgcct atggacartc cagttgagac cctttcaacg gctttccant 840

cgagantttg tttttacaa tcctagggtt caagggaaaga gctttntaca gttatgctgg 900
gttgggtcc aggtccccgg g 921

<210> 34
<211> 1467
<212> DNA
<213> Homo sapiens

<400> 34
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tgctctgttt agtttgcata taaagaaaaa ttaagagggtc ttatgttttc ctatagaact 180
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aaatggat caaaaacatg gaaaaaaa 1467

<210> 35
<211> 2077
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (12)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (15)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (423)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (730)
<223> n equals a,t,g,-or -c

<400> 35

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cangccatgg ccatggcga gaactttcc agtatatgtt gcagaaggag cgagtgaaac 480
cgcaccaact ggcaatttgc cgaccctcac agaagctgt gaaattctg aataagcact 540
acaatcttgc gaccacagtc ccacaggtga acaactttgtt gatctttgaa ggcttcttg 600
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<210> 36
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (366)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> -(37.0) -----
<223> n equals a,t,g, or c

<400> 36

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ccgggtcgag gcaggggcag gtccgggtcc aaagcaagga caccacagct cttccgactc 180
cagcagcagc tccagcgtt cggacacgga tgtraagtcc cacgctgctg gctccaagca 240
gcacgagagc atccccggca aggccaagaa gcccaaagtg aagaagaagg agaagggcaa 300
gaaggagaag gccaagaaga aggaggctcc ccactgaagg gcctggacaa ggctcattaa 360
acttcntctn tgccaaaaaaaaaaaa 384

<210> 37

<211> 468
<212> DNA
<213> Homo sapiens

<400> 37

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tctccaataaa atcttagaa ttttcgagga aaaaaaaaaaaaaaaa 468

<210> 38

<211> 1095
<212> DNA
<213> Homo sapiens

<400> 38

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agaccatcac gggaaattct gctgtgtta ttacccatt caagttgaca actgaggcaa 180
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tcatccccac ttagtcacg agatctttt ctgctaactg ttcatagtct gtgttagtgc 600
catgggttct tcatgtgcta tgatctctga aaagacgtta tcacctaaa gctcaaattc 660

<210> 39

<211> 1757

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (596)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (647)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (648)

<223> n equals a,t,g, or c

<400> 39

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ctggtgtttt attttgtgt acatttactc aacttgtcca tttagtattta actatntcca 600
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 ggattatgaa aaagaaaa 1757

<210> 40
 <211> 1945
 <212> DNA
 <213> Homo sapiens

<400> 40
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 aagcccttgg aaagatgtcg cgttccgaac ctgtgcctaa tacacgcaag ggcgcgtgtcc 1860
 cggccaaaccc cggccctttaaa cggccacaaat aaagagcatt gtaccggcca agtacgacgc 1920
 gggccgcgaat taccggaccg gtaac 1945

<210> 41

<211> 588
<212> DNA
<213> Homo sapiens

<400> 41
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ttgaatctga agtttgcaga tatgcctata gatTTTgga gtttaccact ttcttattct 180
gtatcatcaa tgtaatattt taaaattacta-tatatgttac cattttctg_gatTTtagtaa 240
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catttttttc attactgtta tatttaacc tgactgactg atctaattgtt attagtattg 360
tgaataatca tgtgaaatgt tttgagacag agtactatat ttgtgaaatat aatttttatgg 420
ttttttcac tttagaacctt tctgtgtgga aaactaagaa aattgcttgc tgctgtataa 480
tctggcattt attgttagatt aaagcttattt tttctgtgaa taaaacgtat tcaataaaaat 540
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<210> 42
<211> 1568
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (104)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (112)
<223> n equals a,t,g, or c

<400> 42
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aaggaaagttt ggagaagaaaa accgagatata gaaaatatca tgTTTgggtt ggagataaga 240
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caaacatattt ctttgggtta tatttataca tatgtgaaat aaatatacta tcaaaaaggattt 960
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aaaactatca agaggctgt tagacaaattt tatattctga aacctcaata agaaagcattt 1140

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agtagttatc aaattaaga gataaagcaa tcagaatgtt tggattttct tctatcttaa 1500  
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ggggaaaaaa 1568
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<210> 43
<211> 1060
<212> DNA
<213> *Homo sapiens*

<400> 43
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cccggaggag tcataaagcg agatggaa ataaaaaacag gtgacatcccgttgaatgtg 180
gatggggtcg aactgacaga ggtcagccgg agtgaggcag tggcattatt gaaaagaaca 240
tcatcctcga tagtactcaa agctttggaa gtcaaaagat atgagccccg ggaagmctgc 300
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agaatttagat gtggtgatattcttcttgct gtcaatggta gaagtacatc aggaatgata 600
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<210> 44
<211> 1344
<212> DNA
<213> *Homo sapiens*

<220>
<221> misc feature
<222> (144)
<223> n equals a.t.g. or c

<220>
<221> misc feature
<222> (163)
<223> n equals a t q or c

<400> 44
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 accaacaacc actggccca gggnaccac tggcctcca ggncytccag gcccattggg 180
 tccttggg ctcctggcc ccacagggtgt ccctgggagt cctggtaca taggacccc 240
 agccccact ggacccaaag gaatctctgg ccacccagga gagaaggcg agagaggact 300
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 tcagctggag ctctggcca gamgggtcam cctctggaa gccatcatct ggcagaacc 480
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 ctgagggtgg tggcggccca tgaggcagac cagggcagcc ttccctccct acctggactc 660
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<210> 45

<211> 892

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (890)

<223> n equals a,t,g, or c

<400> 45

ttgagaagtt ggatgaatat atatataagac acttctttgg tcacactttt tccctccat 60
 atggacccag tcgacctgtt aaaaagcaac gtatggtaaa tattgaaaac tccaggcata 120
 gaaaacaaga gcagaaggcac ctccaggccac agccttataaa aagggaaggt aaatggcata 180
 aatatgtcg cactaatggg agacaaatgg caaatcttga aatagaattt gggcaattac 240
 cttttgttcc tcaataactgtt ttcacaattt agttaaatta gacaaactgttta agagaaaaat 300
 ttatgttttgc tataatgtttt ggtattttttt ctaatgaaat taccaagatg acaatgtctt 360
 ttctttgtt tctaagtatc agtttgataa ctttatattt tccctcagaa gcatttagttt 420
 aaagtctact aacctgttcc ttcctgttgt ttagcttcgt tgaattttttt ttgacactgg 480
 aaatgttcaa ctgttagttttt attaagaag ccaggcatgc aacagatttt gtgcgtgaaa 540
 tgagacttcc ttcctgttgtt agagctttaaa gcaagctcag tcatacatgtt caaatgtttaaa 600
 ttaacactgtt tttttgtttt aaatttgcag cagagcttga gaaaagtata ttgttcttgg 660
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 gccctctgac ttgtgaagaa tttgcttccctt tcttaagatc ttgctgactt gttttcttgg 780
 gaaattttttt gcacatctgtt atatcggtt agaaaacaata aaactacacc atgaggaaaa 840
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaagg gggggggcccn ga 892

<210> 46

<211> 496
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (496)
<223> n equals a,t,g, or c

<400> 46
aattcggcag agtcggagtg tggtacttct cctagttca gtcaggcttc atacgctatt 60
gtccctcccc taagttccc ttttgttgt ggtagagca gccagcggtt acagaatgg 120
tttggaaaga gggagtacc actggaccc caaggaagcc acgtgcagac atctacaacc 180
ttcgatctcc tgacgagttt attgttgcc aaaaccaggc ttgattgaa ccaggatgaa 240
tgccgggttt ggaagtagaa tatatatata catataaaaat taaaaactggc gatggaatat 300
gagaggagcc ctctggaaag aaaaggacag acctgtgct ttcatgaaag tgaagatctg 360
gctgaaccag ttccacaagg ttactgtata catagcctga gttaaaagg ctgtccccac 420
ttcaagaatg tcattgktag actttgaaat ttctaactgc ctacctgcat aaagaaaata 480
aaatttta aatcan 496

<210> 47
<211> 1229
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (764)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1165)
<223> n equals a,t,g, or c

<400> 47
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tctaaatatt gcaatcttga ttttactat taaatttgg aattgtcagt tctggctttt 120
ttgcataaaag agttggtcca ttaacttgcc aatttgaagc ttctaaacttag atattcccta 180
ctgaaagttt tggatgggtt tttagttgtt ggagcagtct tagctgggga caggtaattt 240
acaacggcag agataactttc tttccctagg attctaagtc tgtaatccac atccctcaatg 300
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gtgtcattag ccctttgccc gtttacctta gggcttttg aaggagaaat ggatgggaga 480
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gttccaagcc ccaaaggtaa tctagaacca ctcgataaca ccaataaaaa tatttatttc 600
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acaggtgacc attgtgaggt agawattttt ktctaaawttt ccagatgagg aagctgagac 720
cctaaaaggt taggtgacag gttataacaac ttggagtgtt ggangaggag agaggaacct 780
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tggtttcatt atattcctct aacagggttg aaccgattgt ttttgagtac ttgtttcaaa 1140
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-<210> -48

<211> 1411

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1410)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1411)

<223> n equals a,t,g, or c

<210> 49

<211> 1685

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,q, or c

<220>

<221> misc feature

<222> (344)

<223> n equals a.t.q. or c

5220>

<221> misc feature

<222> (1606)

<223> n equals a.t.q. or c

<400> 49

cgctnttccc ccccacaccc gtgtggccag ggatccccgc atggcccatc tttagaaaactc 60
aactatttgg tggatgctaa acacttcact tcagggcaatc ccaaggcatt tgctccaggg 120
tatccgatga gattacagct gtaagcttg ctttccattt cataacttgc tgcagcta 180
gttaccaccc ccatgctgaa gagtaaagca aagtgcgcgtg gttcgcgcgt ggaatccacc 240
cccagcactc tgctcgact ggagcgttca agtccgggtt tgcgagaaca gactaggact 300
ctcttgctgc ctctaattgc atttcactgt caccctcccc agtnttctga tgggtgtgc 360
gtgaggagaa gatgaggta ggactgagaa gtgcagaagt tggaaacagt gtaaggctgt 420
tttaaaataa gatgtttgt ttaataata tgctcctggc acaaagctag gagtaaatgt 480
gactccaaag ggagttcagt taatctctga aatgcacaaa acctagctat ttctccctc 540
tcatcacagt ctgagtcgtt ccattgtca ccccaattct ctggggacat aaaaccaggc 600
tggaaaggga ccaggaagtt tggaaatagtg acatatcatc cactagtccc aaggggctaa 660
gaatagttag tttattctgg aaggaactgg gaagcttagt ctaatttagt cttggggatg 720
acctatgc当地区 ccacaccgt tatgaccatc cttagaggg ccctgagcac cagttgtac 780
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atgagcttgc atccaggggag gaatacctcg gtgccttaac caccttagtt ataacacatt 1680
tctta 1685

1685

<210> 50

<211> 660

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (515)

<223> n equals a,t,g, or c

<400> 50

cggcacgcgt gggcctactt tcacgcttcc tccccctccccc ctcctccctt atcccttcgc 60
tttcgtctt ttccgtcgag gccgaccctt gagttgtgag tctgggtct gggtggtaa 120
aaagagccct tgaagctgga agacgggaga ggacaaaagc atgtcttccc ttccctgggtg 180
cattggttt gatgcagcaa cagctacagt ggagtctgaa gagattgcag agctgcaaca 240
ggcagtgggtt gaggaaactgg gtatctctat ggaggaactt cgccatttca tcgatgagga 300
actggagaag atgattgtg tacagcaacg caagaagcag ctagcagagt tagagacatg 360
ggtaatacag aaagaatctg aggtggctca cggtgaccaa ctcttgatg atgcattccag 420
ggcagtgact aattgtgagt ctgggtgaa ggacttctac tccaagctgg gactacaata 480
ccggggacagt agctctgagg acgaatctt ccggncatcaca gaaaataattt rggattcctga 540
tgaatgatgat gatgtcctca gtattgattc aggtgtatgct gggagcagaa ctccaaaaga 600
ccagaagctc cgtgaagcta tggctgcctt aagaaagtca gctcaagatg ttcagaagtt 660

<210> 51

<211> 1572

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1555)

<223> n equals a,t,g, or c

<400> 51

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actaaagctg aaatgccaca aacactaaaa gtataaatat gtctgatttt taaaacacat 120
aagctttgct cttttaggcag gaatgatctt ttccaaatcat tagcacaata tttaaatatc 180
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tatctgcact taggtataacc tctttatgcc aataatgatt ttaatgaagg ctcttttcag 360
atgtacccctt atgaaggaaa tatctgctt gtgtatatgc cagttagaat actgggttct 420
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catatgtatg tattatatat ccacatataat agttttccctt gattaaatgg atattaaaat 660
aatttgcgggt gcttcaggac tttttgcttca tataattttaa tattttgtttt ttatagcaag 720
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caratattca ataaaatggc aacctgttaa aaaaaaaaaa aaaaaaaaaa acccnaagg 1560
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<210> 52
<211> 635
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (632)
<223> n equals a,t,g, or c

<400> 52
gctgctccag ctgttcaag gtatccaga cgcaagatgg ctgtcccttc taaggaatat 60
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gttccaagg cccgcaagaa gtacaaagtg gagtatccta tcatgtacag cacggaccct 180
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aaatgctgcc attaaagaat tataggggtt taaaaactct cattcattt aaatgactta 540
ccttatttc cakttacatt tttttctaa atataataaa aacttacctg gcatcagcct 600
catacctaaa aaaaaaaaaa aaaaaaaaaac tnggg 635

<210> 53
<211> 1367
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (106)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (958)
<223> n equals a,t,g, or c

<400> 53

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taccataacc aaacattttg tgcgtgtctt attgttgcgt cgatantctc ctttgggtgg 120
aacacagtga agatcgacat gagtgcagcc cgaggagatc ctcttccaat ttttccattt 180
ggattagctg catttgcac cactttgtt gccttggat tagctttagg aacaaccata 240
gctgtggaa tggtttttt tattccagatg aaaataatc tcagaaacaa aacttcttatt 300
gagtcatgga ttgaagagaa ggctaaagat cgaattcagt attatcaact agatgaagtc 360
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gaagggtttt caagaataag ggggtgggtc cctagaaaaat gtgtggaaaaa gtgtccctgt 780
gatgctgaaa cagatcaagc cccagagggg gagaagaaaa atagatagct gctgttaaaa 840
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tatttcttat atgatattct agatactata gaactcaatt tgcagattc agtataacct 1260
cagatttgc tacctgtctt taaaaatgc agatttgc aaatcaaata aagatcaatg 1320
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<210> 54

<211> 378

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (14)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (29)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (363)

<223> n equals a,t,g, or c

<400> 54

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aaggccagggc ggwgttcara ggaggtggac ggccagcacc cggcccaaga ggaggtcccg 180
gaatgcggcc agacctctgg cccagagcag aaaataggtg tgggagccccc aggaggaaaa 240
agccarytgg agaggaagca gagwtggaaa aggctacaga ggtgaagggg gagagggtgc 300

aaaatgaaga ggtgggacct gaacatgaca gccaaagaaac aaagaagctt gaggagggag 360
ctncagtgaa ggcgaccc 378

<210> 55
<211> 1058
<212> DNA
<213> Homo sapiens

<400> 55
tcgggtatga ggctggact aagccaagg attcaggtgt ggtgcgggtg ggaactgagg 60
aagcgcccaa gctttttgt tctgaactcc cactgcgtt tggattcctg agatggat 120
gactgtatct tgattaccgg gagtttcaa gatggcagca tctatgcatt gtcmgcccag 180
tccttcctcta gaagatgcaa aactcagaag accaatggc atagaaatca tagaaaaaaaaa 240
ttttgactat cttagaaaaag aaatgacaca aaatatataaa caaatggcga catttggAAC 300
aacagctggg ttctctggaa tattctcaaa cttcctgttc agacgctgtc tcaaggttaa 360
acatgatgct ttgaagacat atgcatttgcatt ggctacactt ccattttgtt ctactgtgt 420
tactgacaag cttttgtta ttgatgtttt gtattcagat aatataagca aggaaaaactg 480
tgaaaaacta agctcaactga ttggcatagt ttgtgggtt ttctatcccc gttctttggc 540
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aagggtttta atccatttggaa tgacgcggg tcaaaacacaa atgaaattaa tggcgattcc 660
tcttagtctttt cagattatgt ttgaaatattt aatggtcta taccattatg cagtatttga 720
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tgaacaaaata atttggcttg tgcctttgc ctggtatata gcaaaatactc aaaaagtatt 900
caataattca atcaataaaat ataagtttca tcttacacgt aagatacagg tcttatctcc 960
tgatggtgtg tccattttgc ctggtatata acagataata aatatccagt gtcaataaaat 1020
gtaacaataaa aagtttcatc tttcctctttt gtatgtgg 1058

<210> 56
<211> 682
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (667)
<223> n equals a,t,g, or c

<400> 56
gggnccggaa catattccct tactaaaaag attgcatttgc tgaatttgc taaggaaaaa 60
aaaaatttgc tcaagtccat taatacaattt atacattaat tatattacat taatacaata 120
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tttcattttc ttggtaagc agttgtctcc taatattatc ccatatgcatttgc 240
tggcccaag cagtttactg tacttcacta gatgggtac ctgctctccc ctggacttct 300
ttttcaatat tcttagccctt cctagatgta aatcttacc tccttggtag tggaaattttaga 360
tataagccat gatttgaga gggaaagaaat ctggaaatact taatttcatt taatttatcta 420

tgctgatgaa tgcctgtatc attgttaata aaggagaatt gaaaatactc atttctactt 480
tctgccctca aatttctgtt tctatctcaa cttagcaaga atcagcaggg tgcgtgaygc 540
catttaagc tgcttcacat cagactgaaa tcctaattac agttcataag taaaacagac 600
taattcmatg ggcaataacct ttktawagg tccygtgctt aaaggaggca agtataaaatt 660
ttcccantaa ggaatccccg gt 682

<210> 57

<211> 644

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (27)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (458)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (619)

<223> n equals a,t,g, or c

<400> 57

ggagnctggg cctgtgcggc ggccgcngta gcgcgttggaa aggcgcacgg ggcgaagatg 60
gcggcgacg acaggaggcg ctgagggagt tcgtggcggt gacgggcgcc gaggaggacc 120
gggcccgtt ctttctcgag tcggccggct gggacttgca gatcgcgcta gagctttta 180
tgaggacgga gggatgaag acattgtgac catttcgcag gcaaccccca gttcagtgtc 240
cagaggcaca gcccccaactg ataatacgatg gacatccttc agagaccta ttcatgacca 300
agatgaagat gaggaggaag aggaaggcca gaggtgagtc ttctagaggg ggtcagggggg 360
acagttcaca gggaaatgtc gggtaatgtg taaatcacct agaacaggac ctgtaaaac 420
atgtttgggtt tattgttagc cattactact gtgggctngt ctgtgtgggt tataatcttag 480
gaagtctctt ctactccttg tagcttagaa gtgacccctg ttccgttact taatgttattt 540
attgaggaat attaggggag gaaaaccaag gaaaagatct agcattccca cttttggta 600
ttgactaaaa aggatttgnaa aatcgatggtaaaaagaagg tgtc 644

<210> 58

<211> 766

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

222 (760)

<223> n equals a,t,g, or c

<400> 58

gggtcgaccc acgcgtccgg aatgttttg tgaataaaatc tgttcttcag caaccctacc 60
tgcttctcca aactgcctaa agagatccag tactgtgac gctgttcttc catcttact 120
ccctggaaac taaccacgtt gtcttcttc cttcaccacc acccaggagc tcagagatct 180
aagctgctt ccatctttc tcccagcccc aggacactga ctctgtacag gatggggccg 240
tcctcttgcc tccttctcat cctaattcccc cttctccagc tgatcaacccy ggggagttact 300
cagtgttctt tagactccgt tatggataag aagatcaagg atgttctcaa cagtcttagag 360
tacagtccct ctccatataag caagaagctc tcgtgtgcta gtgtcaaaag ccaaggcaga 420
ccgtccctctt gccctgctgg gatggctgtc actggctgtg ctgtggcta tggctgtgg 480
tcgtggatg ttcaagctgga aaccacctgc cactgccagt gcagtgtggt ggactggacc 540
actgcccgtc gctgccacct gacctgacag ggaggaggct gagaactcag ttttgtgacc 600
atgacagtaa tgaaaaccagg gtcccaacca agaaaatctaa ctcaaagtc ccacttcatt 660
tgttccattc ctgattctwg gtataaaaag acaaactttg tacctaaaa aaaaaaaaaaa 720
aaaactcgag gggggggcccg qaamcaattc qggctataagn agagcq 766

<210> 59

<211> 2361

<212> DNA

<213> Homo sapiens

2203

<221> misc feature

<222> (1174)

<223> n equals a + s or s

<400> 59

<210> 60

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (129)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (130)

<223> n equals a,t,g, or c

<400> 60

aattccggcac gagccccagat ggccgtggag gaccaggccg ccacactgga gtataagacc 60
atcaaggaac atctcagcag caagagtccc aaccatgggg tgaaccttg ggagaacctg 120
gacagcctnn cccccaagaat tccacagcg gaggcctccc tgggtcccc gggagcctcc 180
ctgtctcaga cccggttaag caagcggtcg gaaatgcacc actcctcttc ctacggggtt 240
gactataaga ggagctaccc cacgaactcg ctcacgagaa gccaccaggc accactctca 300
aaagaaaacaa cactaactcc tccaattcct ctcacctctc cagaaccagg agctttggca 360
ggggagacaa cccggcgccc gccccgcaga gggtggtactc catccagggtg cacagctccc 420
agccatctgg ccaggccgtg actgtctcga ggcagcccag cctcaacgc tacaactcac 480
tgacaaggtc ggggctgaag cgtacgcccct cgctaaagcc ggacgtaccc cccaaaccat 540
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tcctcctctc tgggacacag gggtaactcac gaaaaactggg cccgctgggtt tggtaaggt 780
ttgcaacgjc ggggactcact cttcattctc ttccctcact ttcccccaca ccctacaaca 840
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ccccatcccc caccacccmca cacacacaca catgcacaca acacatacac acacacqcac 960

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aaaaaaaaa agaattcatt gataattcta actcagactt taacaatggc agaagttac 1140
tatgcgcaaa tactgtggaa tgccccccag ttttacagct ttctgttgca gcagataaat 1200
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ctttccaaa tatcatccctt tgaacagctc ttcagaaagc ccattgaaag ttttacaat 1380
taacgtgaaa tccattaact ggaataattt agtttcttta ttttacaat aaattcactg 1440
agtaaaataaa aaaaaaaaaa aaaaaaaaaa aa 1472

<210> 61

<211> 1672

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (884)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1583)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1645)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1663)

<223> n equals a,t,g, or c

<400> 61

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aagcgcagct cccgacgcaa tggacccggc gctggcagcc cagatgagcg aggctgtggc 120
cgagaagatg ctccagttacc ggcgggacac agcaggctgg aagatttgcc gggaaaggcaa 180
tggagttca gtttccttggaa ggccatctgt ggagtttcca gggAACCTGT accggaggaga 240
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caccctgtgt gtaagcagaa cctccactcc ctccgctgccc atgaagctca tttctcccag 420
agattttgtg gacttggtgc tagtcaagag atatgaggat gggaccatca gttccaacgc 480
cacccatgtg gagcatccgt tatgtccccca gaagccaggt tttgtgagag gatttaacca 540
tccttgggt tgcttctgtg aacctcttcc accaagacca acctggtcac 600
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ccgcagcatg accccggttt atgccaacct tcgaaaagca gtgaagcaat tccatgagta 720
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tgatatacgt ctttatgc cgaaaaatat ttatTTCC taaaaaaagg 1260
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cgaggcagg gagggctctgt nctttcca gggccctggg cagggccatc ctggccattc 1620
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<210> 62

<211> 1540

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1265)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1468)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1507)

<223> n equals a,t,g, or c

<400> 62

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tttctgaaaa ggccactcac gtgaacacta gggatgaaga ttagtrtacc cctcttcata 120
gagcagccta cagtggacac ttagatattt ttcaggagct cattgcacag gggccgatg 180
ttcatgcagt gactgtggat ggctggacgc ccctgcacag tgcttgtaag tggataata 240
ccagagtggc ttcttttta ctgcagcatg atgcagatata caatgcccac aaaaaaggcc 300
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tcctgatgaa ccgttacgtc aaaccagggc tgaaaaacaa cttggaaagaa actgcattt 420
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attctcacc tcagtcttaa caattctagt aattttcata agtttctaaa taccagtgcc 540
tcctgtgtgt gagatgtatt cccataatca aagttgacgt caaacatctt actacaaaaa 600
ttcagtgaca ttcattataa cattttcca agtgaattgc ctgacttta tgcataatg 660
tatttggaaat taatttgcataatcttta ttatTTGT ggagttgtg attttttat 720
cagaaaataat tttaatgtgt gtatacttaa aaacttgaca cgggttgatc agaaactgg 780
atttttgggtg ctgatacaag agaaatgtat tttaaatat cccacatctt ggatcttgc 840
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gcaaagtgac agggggaaag gaatttagtct aagagtaagg ggatgattat tatrttgagg 1440
staaaaaccac aaagtggctc aggcttnaa aaaaaaacac tgtggataat gacaaaaagc 1500
ataagtnaaa atatttggaaa aaaataaaagt acaagaatg 1540

<210> 63
<211> 1044
<212> DNA
<213> Homo sapiens

<400> 63
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caatgcAAGA acggcaAGAT gaACTGCCAT gaggGTGTA gAAAGGTCAc agATTGcAGG 120
gacacAGGAA gttccAGGGC acccaACTGC agatATCGGG ccATAGCAG cactAGACGT 180
gttGTCATTG CCTGTGAGGG taACCCACAG gtGCTGTGc acTTGACGG ttagATGCCA 240
ccATGTAGGG attATCGCGA gtGGTGTACC ttACACTTAC tcCTTAAATA gcAGTGAgtA 300
atGCAATTG A GCTGTCCTAG gCTCTGTCTC CTCAGCTCAT ttCCtACTCT ttttCTCTAT 360
ataACTCATT CTATTAATAA CATTGCACCA aAGAGATATG gagACATAAA CCTGTAATGA 420
atGAGGCTGG GCTTTCTGT aATAAGCTTC CTTTATAAT ACTGGTCAGC ttagCTCTCT 480
cAGATCCTAT CCTGTGGAAT TTAGTTATT TGtGTATT TGtGTATT caAAACATTc 540
aaaATGCTT CATCTATGTT TATCACATT TAATACCAcA GCACTTAA TGATGTCACT 600
acATATAGAA GCTCAAAGTT AAGGGATTG CTGAAGACTG TAAAGTTAAT ggaAGAATTG 660
agACAaaaAT CCAGTGTAGC TGGCCACTTA TCCAGGGCTT tttCTACTTC ATCACAAGGA 720
atGTTTGAAT AGTGTCTGCT TTTTTATCC TAAAAATTCA CCTGTCAAGGG AGGCATTAAA 780
aATTGGAAT TGtATGCCAG CAAAATGTGA GCTCTGTATT TTTGGCATT CTTATGTTG 840
gTTTAATAA GATTAAGAAA ATGATACTGG GAATTTCTT TTCCtGAAAGA CTTGAATCA 900
CCCTAGTAAG TCAAAGTACT AAAAATGTA CTAGATCATT AAGACTTATG TGCTCTTACT 960
GATTGAAAGA TTTTTATGT TTCCtGTa ATAAGGAGC TAAACCGAAG GTACCTGAAA 1020
aaaaaaaaaa aaaaaaaACT CGAG 1044

<210> 64
<211> 851
<212> DNA
<213> Homo sapiens

<400> 64
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ctggAAAGCTG CCTGTGCTAA gaccACCCAG ctgtccCTGG gttctcatcc tagggcCTTC 180
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ggaAGACCCA ggtggccca tcaaAGGAAC ctgggggAGG atgcAGGAGG ctGAAGGGAT 480
gcacccctggca ttctctcac tGtGCTCTTA ccgcAtcAGC aACCCCCAAC ttttggcCT 540

actctgcccc ccatgcgtga ataccctgct tggatgctgt gctttccgg tttgtctcta 600
agcccctttc tccaggccat gttggttcc ctggcctctc agtgcctaa ctggagccca 660
gagtgccttg ttctgagcca ggagacggct gagcactgac cctccacacc taagcgtcct 720
ttacattaac ttattggctc tgtataaacac ctggccat tgccaagtgg ctgtgcctc 780
agctacagag ctggaaattgt gtggggtta gtgctaaata cttcaataaa gtctgtttt 840
tgtgattggc t 851

<210> 65

<211> 2793

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (2793)

<223> n equals a,t,g, or c

<400> 65

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gaatgtctaa atattgtta cattaggatg atacatgtaa attaaagtta catttggta 120
gcatacgacaa gcttaacatt gtagatgtt ctcttcaaaa atcatctaa acatttgcatt 180
ttggaaattgt gttaaataga atgtgtgaaa cactgtatttta gtaaaacttca tcacccccc 240
acttccttat agtttgaact tttagtttt tgtagtccc aaacagttgc tcaattttaga 300
gcaaatttaat ttaacacctg ccaaaaaaaag gctgctgtt gcttattcagt tgctttaaa 360
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gctctgaaaa ttaccgcgtt tagtaattat agtggctta taaaaacatg caactctttt 480
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aaccataatata ttgatatttt taaaacattt ttacatataaa gtaaaactgcc atctttgagc 600
ataactacat taaaaataaa agctgcataat ttttaatca agtgtttaac aagaatttt 660
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<210> 66
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (108)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (278)
<223> n equals a,t,g, or c

<400> 66
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attaatactg atgtgaatgg atgcattttgt tttgcagttgg tgactggcct aggcagggtt 180
gggatctgtg aaagaattga ttcatatca aaattattcc ataaagttaa aaagttacac 240
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aag 303

<210> 67
<211> 1410
<212> DNA
<213> Homo sapiens

<400> 67
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gtgtgacccat gaatttggca atgacaaggc caggagccg agcgtgggtg gcagggtggcg 180
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<210> 68
<211> 1024
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (7)
<223> n equals a,t,g, or c

<400> 68
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tctt

1024

<210> 69

<211> 1848

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1761)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1844)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1847)

<223> n equals a,t,g, or c

<400> 69

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catcaagtac atcttgaacg tcaccccca tttgccaat ctcttgaga acgcaggaga 180
gtttaataac aagcaaatcc ccacatcgga tcactggagc caaaaacctgt cccagtttt 240
ccctgaggcc atttcattca tagatgaagc ccggggcaag aactgtggtg tcttggtaca 300
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caatctgtcg atgaacgatg cctatgacat tgtcaaaatg aaaaaatcca acatatcccc 420
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aaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1848

<210> 70
<211> 2682
<212> DNA
<213> Homo sapiens

- - - - -
<220>
<221> misc feature
<222> (647)
<223> n equals a,t,g, or c

<400> 70
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tagacagact atgctttt ctgccaccca aactcgaaa gttgaagacc tggcaaggat 180
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ggatggctt gaacagaaga accgaaagaa gaagctttagt gtctctttt catcttgtat 300
gtctgtgaaa taccactatg agttgctgaa ctacattgtt ttgcggctt tggccattca 360
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aaataattac ttcaatgttgc aaaaaaaaaaa aaaaaaaaaaa aa 2682

<210> 71

<211> 412

<212> DNA

<213> Homo sapiens

<400> 71

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ggaccgcccc aaccctcgga gccccccact cagtaggtct gaaggcctcc atttgtaccg 180
aaacaccccg ctcacgctga cagcctccata ggytccctga ggtaccccttc cacccagacc 240
ctccttcccc accccataag ccctgagact cccgccttrr acctgacgat ctccccctt 300
ccgccttca gggtcctcct aggccgctcag aggccgctct gggtgggtgc ctgcagtccc 360
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<210> 72

<211> 1361

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (46)

<223> n equals a,t,g, or c

<400> 72

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<210> 73

<211> 928

<212> DNA

<213> Homo sapiens

<400> 73

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ggtgcagag atagcacaca cctacaaggc cgacagagag aagtacaaca gactagcaag 180
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tggtgccatt ttcagcaatt acggcttga cagtgcacc tctttatgc caaatcagca 420
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cagtgcacg tggtaattt tctgccttc acaccaagaa agcagcaaag tgaaaat 840
tcaaggatac aaaggcacat aacamccca taagragatg attaagg ttttagaagca 900
agagcaaaat tttgaaaacc tctaggag 928

<210> 74

<211> 1186

<212> DNA

<213> Homo sapiens

<400> 74

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<210> 75

<211> 933

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (791)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (794)

<223> n equals a,t,g, or c

<400> 75

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atgaagagaa actggtagcc tcactatggg gaggcagagag atgtttacga gtttttagaaa 120
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tgaagaacctt gacctccaat aaaggtatata ttactttgaa tggtgatattt aaattgaaga 900
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<210> 76

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 76

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<210> 77

<211> 1802

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1680)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1747)

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<220>

<221> misc feature

<222> (1757)

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<221> misc feature

<222> (1800)

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<210> 78

<211> 995

<212> DNA

<213> Homo sapiens

<400> 78

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<211> 1215

<212> DNA

<213> Homo sapiens

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<211> 2660

<212> DNA

<213> Homo sapiens

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<211> 1790

<212> DNA

<213> Homo sapiens

<400> 81

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<212> DNA
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<211> 1746
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<400> 83

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<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (176)
<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (711)

<223> n equals a,t,q, or c

<400> 84

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tgagataaaa ggggatctca acaaccctca ggattcagaa gtgttaaac ac tcctgnaccc 180
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tatcaaatcc gaatattaga tcctttcatt atcagaacag cagttatgaa actgcttcat 1380
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<210> 85

<211> 968

<212> DNA

<213> Homo sapiens

<400> 85

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tgaataccca tcttctagtt taaagacaga gacatcccat ctgaaaaatg ttaacttg 180
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caaaggggcaa atttaaaac ttcaagtctgg gtgaaagatt tgctagttt acagaaaagat 600
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ctacactata tgggtctgg agtgttgaac aaatttttt tagttctaa gttgtaatct 780
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gtacaattt aagtggtagc agtttctgtc tgccatggc tgaaatattt tgatgaactg 900  
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<210> 86

<211> 3068

<212> DNA

<213> Homo sapiens

<400> 86

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gtctgaaaat tccagtaca gtgattcatc ttgtggttgg actgtcatca gtcatagggg 180
gtcagatata gaaatgtga attctgtac cccccactgac agctgtgac cccggccca 240
atgttcatct ttagagcaag aggagcttca agcattgcag atagagcaag gagaaggcag 300
ccaaaatggc acagtgcta tggaaagaaac tgcttatcca gctttggagg aaaccagctc 360
aacaatttag gcaagggAAC aaaagatacc cgaagacagt atctatattg gaaactgcc 420
tgatgattct gatattgtta cccttgagcc acctaagttt gaagaattt gaaatcaaga 480
agttgtcatt gttgaagaag cacagagttc agaagactt aacatggct ctccctctag 540
cagccagttt actttctgtc agccagaaac tgtattttca tctcagccgt tgacgatga 600
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aaaaaaaaa 3068

<210> 87
<211> 2230
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2227)
<223> n equals a,t,g, or c

<400> 87
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ttgcctacct gagcctcagc cctgtatttG tcatcgTCgg ttcgtgacc ctcatcatat 180
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cacgtgaaca aaatggGAAG gagCCGTGAG gagaggAGTg aggcaACAGG caccCGAAGT 1620
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<210> 88
<211> 1163
<212> DNA
<213> *Homo sapiens*

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<220>
<221> misc feature
<222> (159)
<223> n equals a,t,g, or c
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<400> 88

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caatgctgaa ttatccgtta gat 1163

<210> 89
<211> 1939
<212> DNA
<213> *Homo sapiens*

<220>
<221> misc feature
<222> (20)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (31)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (33)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1609)

<223> n equals a,t,g, or c

<400> 89

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ccgctctaga gatccctc 1939

<210> 90
<211> 2032
<212> DNA
<213> *Homo sapiens*

<400> 90
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ggtgtggcg gagaaaaggg gaagagtcat cgccgtcg ggctaggata tgatgggtga 120
gagggtgtcaa accaaattct ctcgggttgg aaacggagaa aatctaaaaa tgaggatgtg 180
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tttctgagct aaaactcaac tatagaagac attaaaaagaa atcgtattct tgccaaatgaa 1920
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tcaaaaaaaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aagggggagg gg 2032

<210> 91
<211> 1788
<212> DNA
<213> *Homo sapiens*

<400> 91
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aaggggagtg cgggtcgggg aggaatattc ttttggaaac gtaatatattgg ccttggggct 120
ctccagccct tttaggacttc caatggatc tttagaagcag ccgaaagcagc gtqagqqqcqg 180

cagccaggc cagccacgat ttgaacgctc tgccttgcag ctcttctgga ccgaggagcc 240
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 cagaccagac tcatcgaggc ctgaattgtc ccagcctctg aactttgttc gatTTtatct 720
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<210> 92
<211> 495
<212> DNA
<213> Homo sapiens

<220>
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<222> (402)
<223> n equals a,t,g, or c

<400> 92
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tacatggacg tgagcagcct gagatctgag gacacggcca tntattactg tgccaraagk 420
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<210> 93
<211> 1377

<212> DNA
<213> *Homo sapiens*

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<222> (1367)
<223> n equals a,t,g, or c
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<221> misc feature -
<222> (1371)
<223> n equals a,t,g, or c
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<220>
<221> misc feature
<222> (1376)
<223> n equals a,t,g, or c
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<400> 93

<210> 94
<211> 2819
<212> DNA
<213> *Homo sapiens*

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<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (83)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (84)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (2816)

<223> n equals a,t,g, or c

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<221> misc feature

<222> (2817)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2818)

<223> n equals a,t,g, or c

<400> 94

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<210> 95

<211> 705

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (488)

<223> n equals a.t.g. or c

<220>

<221> misc feature

<222> (682)

<223> n equals a.t.q. or c

<220>

<221> misc feature

<222> (684)

<223> n equals a,t,q, or c

<220>

<221> misc feature

<222> (687)

<223> n equals a,t,g, or c

<400> 95

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<210> 96.

<211> 3472

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (55)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (69)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (3457)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (3466)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (3470)

<223> n equals a,t,g, or c

<400> 96

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<210> 97
<211> 1216
<212> DNA
<213> Homo sapiens

<400> 97
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acctaataatggg agctcaaataatg tgggtgtgtc tctctgtgtg tttgtgtgtg tgggtgcact 180
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<210> 98
<211> 1186
<212> DNA
<213> Homo sapiens

<400> 98
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aaaggcctag accagcctgg gcaacagaga ccatgcttaa aaaaaa 1186

<210> 99
<211> 1120
<212> DNA
<213> Homo sapiens

<400> 99
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<210> 100
<211> 1225
<212> DNA
<213> Homo sapiens

<220>
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<222> (286)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (287)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (288)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1213)
<223> n equals a,t,q, or c

<220>
<221> misc feature
<222> (1225)
<223> n equals a,t,g, or c

<400> 100

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<210> 101

<211> 1213

<212> DNA

<213> Homo sapiens

<400> 101

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cattgttagat ccataccac cattatgtga cattaaagga tcatatacag cgcaatttga 660
acataccatc ctgttgcgtc caacatgtaa agaagttgtc agcagaggag atgactattt 720
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ggtmcccaat tcg 1213

<210> 102

<211> 1564

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1509)

<223> n equals a,t,g, or c

<400> 102

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aaataaaat ttttgaccaa aatccagaaa atggatgag agaaaaataa atccagcta 180
gttaataga tttttaatg tcaatctgat tttagctttt agagagtgt aactagctkg 240
taatgtttac ttttaattcc ttgtttaat gaggcaataa ttgcagat tttgtat 300
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tttatccatg taaaatagct atttattgaa ttttcttttta aaagctggat ttactgggtt 480
tttttttct ctcagttaa acatcttaac agarawtgc ttactgttta tttaaagaat 540
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tattatcaag tgttaagcac aattttata acaaactgtg ataaattctt tttgtttttt 660
tttcctttgc cccattat tcttatgac aaaccaaaaa ttcatggta gcagttgcag 720
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gctagctttt taaatgttta gtttcctct tttcatggc agctgtgaa ttacttgaa 900
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aatcatttcc ttttaattt taaaatgtt gaggctcata aatattttag aacatcagat 1020
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taaaaaatgtt ctaattttt cactaaatgg aggaaactat tagttttattt gttaaatatg 1260
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aagaggaagt tgctattgca ttgatTTAA tatttgtaca taaacactga ttttttttag 1440
cattatTTTGTG tatttggatc actttaatac ctgggttaca gttccagaaa taaaaatctg 1500
gaaatcttta aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa gggcggccgc 1560
tcta 1564

<210> 103

<211> 1457

<212> DNA

<213> Homo sapiens

<400> 103

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cacaaaagcca aggctctgct ctttgaggta aaggagatct tcaggaagtc acctttcctg 180
gtacccaaagg gcagtgttag catcatggat ggatccgacg aaggcatatt agcttgggtt 240
actgtgaatt ttctgacagg tcaagctgcat ggccacagac aggagactkt ggggaccttg 300
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caaactcccta kgggctaccc cacttcctt gagatgttta acagcactta taakctctat 420
acacatagtt acttgggatt tggattgaaa gctgcaagac tagcaaccct gggagccctg 480
gagacagaag ggactgatgg gcacacttc cggagtgctt ktttaccgag atgkttggaa 540
gcagagtgga tctttgggg tgtagaaatac cagtaggtt scaaccaaga aggggaggtg 600
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tcctcttaaa tggtaaactg acttattgca atcccaagac ccatcaatat cagttttttt 1380
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aaaaaaaaaa ctcgttag 1457

<210> 104

<211> 785

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (748)

<223> n equals a,t,g, or c

<400> 104

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agcaatggca ttaagaggtg gggcctttgg ggctggata caggagttag ccactgcgcc 180
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catcccttggg gaccttgagaa agcgtacttc accttgggtt gaggctggg tggggccaga 540
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tcactgcttc tttctccctg ggaagaatgc gtggactctg cctggtgata gactgaagcc 720
agaacagtgc cacaccctcg ccttaatncc ttgcttaggtg tctcagattt atgagacttc 780
tttagt 785

<210> 105

<211> 921

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (40)

<223> n equals a,t,q, or c

<400> 105

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aaacagttgc cccagaaaaga catgtcttgt tttaaagccc agaacctgaa attattatag 120
attttattcg gtaataagga actttgcata tgtaattact taaggatatg aagatgagat 180
tgtcctggat tattaagcac cctaaatgcc atgtacagg tgccttccaa gagaacagaa 240
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ggccacaagc ccaggacac ctggagcccc caggagctgg gagaggcagg aaggatcc 360
ccctagagcc tccaggggga actggaggat gcgtaaagaga cccagaacct ccacagaagg 420
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tgactcagtc tgttcactgg tttagctttt agtggaaaaga taacacaggt ctattgactc 900
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<210> 106

<211> 592

<212> DNA

<213> Homo sapiens

<400> 106

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aagctggcag agatgttctc tagcttagcc aaggcctcca cgacgcgga gggccgcttc 240
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gcagaagccaa taacagcacg gaaktccagg tgyttgtgt cctggtgaaa cttgaggggag 540
caggatgcat tattattcaq aqqtctctq ttttcttqc aqqataaqaa qq 592

<210> 107

<211> 2248
<212> DNA
<213> Homo sapiens

<400> 107

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<210> 108
<211> 785
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature

<222> (769)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (771)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (785)
<223> n equals a,t,g, or c

<400> 108

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tgcgctctac aaataggccc gtgagaaaga tggccggaa ctgcatttcctg ctggctgtcg 240
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tcttcctttaatgctgca gaagctgttc ccaccatgaa ggtaatatgg tatcatttgc 720
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ccaan 785

<210> 109

<211> 611
<212> DNA
<213> Homo sapiens

<400> 109

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agtggtaggt aaggaaggggg ccttaacctc tgctgggtac cagaaggctg catttctgca 180
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tgacctgaaa cttcaagagt accaaagtgc awtcaaagtg gagcctgcatttccac 540
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<210> 110

<211> 664
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (24)
<223> n equals a,t,g, or c

<220>
<221> misc feature
~~<222> (72)~~
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (614)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (616)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (633)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (649)
<223> n equals a,t,g, or c

<400> 110
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tttatagccct ttcccttaaaa tcaagattga gtttaaaattt atagtttgtc ttttgtctta 480
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gtcaataaaac agatctattc ataaaaaaaaa aaaaaaaaaaag ggcggcccgcc tctagaggac 600
cccaagctta cgtnncngtg cattgcgacg tcntagctct tttataggnng tcaccctaaa 660
tttc 664

<210> 111
<211> 4065
<212> DNA
<213> Homo sapiens

<400> 111

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tcccaagtgc ccccggtccc gcaagaaaaga tgattccctc ttggggaaac tcggaggac 180
cctggcccg aggaaaaag ccaaggaggt gtccgagctg caggaggagg gaatgaacgc 240
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ctgatgaagg tattaattga ctggattaat gatgtgttg ttggagaaag aatcattgtg 420
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<211> 1492

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<213> Homo sapiens

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<220>

<221> misc feature

<222> (1491)

<223> n equals a,t,g, or c

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<222> (3730)

<223>-n equals -a,t,g,-or c -----

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 <213> Homo sapiens

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<210> 116

<211> 1320

<212> DNA

<213> Homo sapiens

<400> 116

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<211> 2025

<212> DNA

<213> Homo sapiens

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<222> (1916)

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<222> (1944)

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<210> 118

<211> 1295

<212> DNA

<213> *Homo sapiens*

<220>

<221> misc feature

<222> (1286)

<223> equals a tag or s

2203

<221> misc feature

<222> (1292)

<223> n equals a,t,q, or c

<400> 118

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 gatggtggcg ttgctgtgc tgctctcagc agctgagcca gtaccaggcag ccagatcgga 180
 ggaccggta cggaaatccca aaggtgtgc ttgttcgccc atctggcaga gcccacgttt 240
 catagccagg aaacggggct tcacggtgaa aatgcactgc tacatgaaca ggcctccgg 300
 caatgtgagc tggctctgga agcaggagat ggacgagaat cccagcagc tgaagctgga 360
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 caactggcc ccagaagagc cacaggaaca tcatttcctt cccgcaacca ctccccacccc 1200
 agggagccctt ggcctccagt gcctcccccc gtgaaataaa cggtgtgtcc tgagaaacca 1260
 maaaaaaaaaaaaaaa aaaaaaaaaaaaaaa aaaaanggg gnccc 1295

<210> 119

<211> 1257

<212> DNA

<213> Homo sapiens

<400> 119

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 ttatTTTaat gactatgaga taatgtatat gacagcactt tgagaaaata tcaactgtaa 180
 tataactata aggtttagt attgtctgtt taaaagataa gacaggatgat tcaatgtgga 240
 tggaccctgt ggggtacctg aaaatgtaga tacgtaagaa tcacccctgt catttatcac 300
 atttagaaat atgaaactgc ttaacaggtt tgagcaggtt tagcaagtgt ttgctaaagt 360
 ttagttcaag agctgaatta cttcaggaaa ctagggacca actttttgtt ttaattccga 420
 tcttaaaaaa gtaagaatgt gtactcactc cagaacacag aagctcttcc aaggaccttg 480
 actcaagaag gatgaggctcc tcttactctt ctccatttat ccactatatg cttggccatt 540
 tatcctaaat gtgggtggaa cagactgtt atctgttgat gttgacagtg tctttttaa 600
 cctatgtccct gcatagtttt gttaggttta cagggggagg tggatggcca taaaaccagt 660
 gcactttggg aattactttt ctaggatttc ctaccaggta taaaatgacat tgacatttg 720
 catctttttt ttctttttct aaaaagaata gctgaattta attcacctat tataaaatac 780
 tcaaaagtaa attgcmttgg tggccacttc tgaattatacg ctacatttca ttatgacccc 840
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 gtttgtgtct ctgtcttagc ttgtatcaag ccagtagtag ctcacttcct ttgtaaattc 1140
 ctgcttcagt ctgggatccg taggagtatg tgagaacttc tggaaacgtct ccaactctta 1200
 acagtcaaga tatctatatac atttggawag agttctggkt ttccaaactac taagacc 1257

<210> 120
<211> 397
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (325)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (378)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (395)
<223> n equals a,t,g, or c

<400> 120
ccccagggaaa ataccaaacc taggttaaaa aatagggaag ggaagggaga gaagaaaggg 60
aagataaaga aagcccaacc tccttccaaa atgtcatgag aatcttgagc acatatggtc 120
cttggcatga ccacatgacc tgcaagccc ctgttataga actcattttt atatttcct 180
tagtataaca gttaatataa tatgtcattt ttgttaatag tgtcttttg tcattttact 240
ttttaaaaga ttttattgaa atatacatac aggaaagtgc atctatcata agtgtgccaa 300
attgatggaa ttctaaaatc tttantggta cctgtttagc acatagattt gacacggAAC 360
ataactaaca accagaantc tccgtgtact ccctncc 397

<210> 121
<211> 876
<212> DNA
<213> Homo sapiens

<400> 121
cccacgcgtc cgggaaagtgc ttactcgctcg tctccatgctcg ccgggttcctg ggcgtcttag 60
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cccgggacgt gagccgtcgc gcccaccggg ctagaccggg cgccatcatg ctgcttctgc 180
caagcgccgc ggacggccgg ggacaccgcca tcaccacgc tctgacccctgc gcctctacac 240
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agaaccaaga tcattatgca gttcttggac ttggccatgt gagatacaag gctacacaga 480
gacagatcaa agcagctcat aaagcaatgg tttaaaaca tcacccagac aaacggaaag 540
cagctggta accaataaaaa gaaggagata atgactactt cacttgcata actaaagctt 600
atgaaatgtt atctgatcca gtggaaaagac gagcatataa cagtgtagat cctacttttg 660
ataactcagt tccttctaaa agtgaagcaa aggataattt ctgcgttgg 720
tggtgaaaag gaattccaga tggcaata aaaaaaaaaatgt tcctaaactt ggtgatatga 780
attcatcatt tgaagatgtt gatataattt attcttctg gtataattt gattcttgg 840
gagaattttc ttattnatgtt gaagaagaaa aaaaaaa 876

<210> 122
<211> 1278
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature

<222> (107)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (128)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (149)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1228)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1231)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1262)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1269)
<223> n equals a,t,g, or c

<400> 122

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gaaagataaa aagagttgac gggcgccgac ctgaaggact gcgtcanaca acagcctgag 120
cagcaatnca gcctccccag cgtcaganc tgccggcgcc tgcgtgagag gagggtcgccc 180
agctggcccg tgtccttga gcgcctgctg caggaccccg tcggtgtccg ctacttctct 240
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atgcatcctg ggccgaagtg gaggggccgtg cactccccga ctcgcagcac gtccccagca 600
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 gntacggcnt ggactcat 1278

<210> 123
 <211> 3115
 <212> DNA
 <213> Homo sapiens

<400> 123

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<210> 124
<211> 379
<212> DNA
<213> *Homo sapiens*

<220>
<221> misc feature
<222> (340)
<223> n equals a.t.g. or c

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<220>
<221> misc feature
<222> (344)
<223> n equals a.t.g. or c
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<220>
<221> misc feature
<222> (366)
<223> n equals a.t.g. or c
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actcacagg aacatgctt cagtcaagta cagattgtgt ccactggaaa ggtaaatgtat 180
tgcttttta tattgcatca aacttggAAC atcaaggcat cccaaacact aagaattcta 240
tcatcacaaa aataattcgT ctttcttaggt tatgaagaga taattatttgc kctggtaAGC 300
atttttataa acccacycat tttatatttgc graaaatccn aaangggtgg gggacgcct 360
tgttagngacc ttccaataac 379
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<210> 125
<211> 1267
<212> DNA
<213> Homo sapiens

<400> 125
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cagcggctga ggagggccc cagcagcccc cgaaggccct atcaggacat ggagtatgaa 360
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cctcgcgagt atggcagcca ggagggcaag catgactatg acgactcatt tgaggagcag 540
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caggactatc ggaccgagca agggaggagg aggaggagga rgaggatgag gaggaggagg 720
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agccctgtca cagggctcgg agccaagctc agagaacgcc aatgacacca tcattttcg 1260
caacctg 1267

<210> 126
<211> 841
<212> DNA
<213> Homo sapiens

<400> 126
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gcgtcaata ctttggatt ttaatttcta gatttggcaa ttcttcgtcg aagtcatcat 180
gagcttttc caactcctga taaaaaggaa ggaactcatt cccttgggtgg ttttcatgac 240
tgtggcggcg ggtggagcct catcttcgc tgtgtattct ctttggaaaa ccgtatgtat 300
ccttgcgtca aaaaaaaaaatc cagaaccttggaaactgtg gaccctactg tacctaaaa 360
gtttataaca atcaaccaac aatggaaacc cattgaagag ttgcataatg tccaaagggt 420
gaccaaatga cgagccctcg cctcttttctt ctgaagagta ctctataaat ctatggaaa 480
catttctgca caaacttagat tctggacacc agtgcgtggaa aatgcttcgt ctacatttt 540
agggtttgtc tacatttttt gggctctggta taaggattha aaggagtgc gcaataactg 600
cactgtctaa aagtttgc ttatttctt gtaaaatttga atattgcata ttgaaatttt 660
tgtttatgtat ctatgaatgt ttttcttaaa attacaaag ctttgtaaat tagatttct 720
ttaataaaaat gccatggatca aaaaaaaaaaaaaaa aaaggccggc cgctctagag 780
gatccctcga gggggcccaag cttacgcgtg catgcgacgt catagctctg tccctacgaa 840
g 841

<210> 127
<211> 1172
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (119)
<223> n_equals a,t,g, or c

<400> 127

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<210> 128
<211> 891
<212> DNA
<213> Homo sapiens

<400> 128

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t 2461

<210> 130

<211> 2197

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1381)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (2194)

<223> n equals a,t,g, or c

<400> 130

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<210> 131

<211> 464

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (397)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (405)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (420)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (449)

<223> n equals a,t,g, or c

<400> 131

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<210> 132

<211> 1950

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1941)
<223> n equals a,t,g, or c

<400> 132
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<210> 133
<211> 2093
<212> DNA
<213> Homo sapiens

<400> 133
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<210> 134

<211> 729

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (646)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (665)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (725)
<223> n equals a,t,g, or c

<400> 134

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gacaaggta gacaacaaca ccctgctcaa cgtcatcgcc tgcacccacg tgccctgcaa 180
cacctctgc agccctggct tcgaactcat ggaggcccc ggggagtgt gtaagaagt 240
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caagaccgtc ctcataatc attgctccgg gtcctgcggg acattgtca tgtamtcggc 600
caaggccagg ccctggacca cagcttgctc ctgctgcaaa gaagaaaaaa ccagccagcg 660
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gccantgcc 729

<210> 135

<211> 1189

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (8)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (17)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1160)

<223> n equals a,t,g, or c

<220>

<221> misc feature

<222> (1175)

<223> n equals a,t,g, or c

<400> 135

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